

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 17, 2003, 12:46:44 ; Search time 12 Seconds

(without alignments)
660.165 Million cell updates/sec

Title: MUT127

Perfect score: 957

Sequence: 1 MGGSGSRSLKELLAEYQDLT.....EFQHVISRSPDFASSFKIVL 191

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	957	100.0	191	1	KIP1_HUMAN
2	904	94.5	191	1	KIP1_MOUSE
3	903	94.4	191	1	KIP1_MOUSE
4	340	35.5	187	1	KIP2_MOUSE
5	338	35.3	187	1	KIP2_MOUSE
6	215.5	22.5	177	1	CALB_HUMAN
7	209.5	21.9	174	1	CALB_HUMAN
8	198.5	20.7	174	1	CALB_HUMAN
9	198.5	20.7	174	1	CALB_HUMAN
10	185.5	19.4	169	1	CALB_HUMAN
11	185.5	19.4	169	1	CALB_HUMAN
12	177.5	18.5	170	1	CALC_MOUSE
13	177	18.5	170	1	CALC_MOUSE
14	173.5	18.1	170	1	CALB_MOUSE
15	172	18.0	174	1	CALB_MOUSE
16	171.5	17.9	178	1	CALC_MOUSE
17	170.5	17.8	186	1	FREQ_MOUSE
18	169.5	17.7	175	1	CALC_MOUSE
19	165.5	17.3	189	1	NCS2_MOUSE
20	157	16.4	190	1	APLC_MOUSE
21	151.5	15.8	189	1	H520_MOUSE
22	150	15.7	189	1	NCS1_MOUSE
23	150	15.7	189	1	NCS1_MOUSE
24	145	15.2	190	1	NCS1_MOUSE
25	145	15.2	190	1	NCS1_MOUSE
26	145	15.2	192	1	VIS3_MOUSE
27	144	15.0	192	1	VIS3_MOUSE
28	139	14.5	189	1	NCAH_MOUSE
29	136	14.2	190	1	VIS2_MOUSE
30	135.5	14.2	214	1	TESC_MOUSE
31	135	14.1	192	1	NCAH_MOUSE
32	134	14.0	192	1	HIPP_MOUSE
33	130.5	13.6	172	1	CATR_MOUSE

34	130	13.6	192	1	NCAH_MOUSE	012953	gallus gall
35	129.5	13.5	214	1	TESC_MOUSE	09jk15	mus musculu
36	129	13.5	192	1	NCAH_MOUSE	P29554	homo sapien
37	129	13.5	192	1	NCAH_MOUSE	016982	aplysia cal
38	129	13.5	192	1	NCAH_MOUSE	P49619	homo sapien
39	128	13.4	189	1	NCS1_MOUSE	009711	schizosacch
40	127.5	13.3	172	1	CAT2_MOUSE	012798	homo sapien
41	127	13.3	190	1	VIS1_MOUSE	P28677	homo sapien
42	127	13.3	804	1	KDGB_MOUSE	09y6t7	homo sapien
43	125.5	13.1	195	1	H520_MOUSE	09d869	mus musculu
44	123.5	12.9	801	1	KDGB_MOUSE	P49621	rattus norv
45	123	12.9	189	1	NCS1_MOUSE	006389	saccharomyc

ALIGNMENTS

RESULT 1
KIP1_HUMAN
ID KIP1_HUMAN \$STANDARD: PRT: 191 AA.
AC 099828; 000735; 000693; 099971; 096J54;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Calcium and integrin-binding protein 1 (Calmyrin) (DNA-PKcs
DE Interacting protein) (Kinase interacting protein) (KIP) (CIB) (SNK
DE Interacting protein 2-28) (SIP2-28).
GN CIB1 OR PRKDCIP OR KIP OR CIB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Yuan O.;
RT "SNK, a Ser/Thr protein kinase, associated proteins."
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA MEDLINE=98040126; PubMed=9372844;
RT Wu X., Lieber M.R.;
RL "Interaction between DNA-dependent protein kinase and a novel protein,
KIP."
RN [3]
RP SEQUENCE FROM N.A.
RA TISSUE=Fetal liver;
RL MEDLINE=97184102; PubMed=9030514;
RT Naik U.P., Patel P.M., Parise L.V.;
RL "Identification of a novel calcium-binding protein that interacts
with the integrin alpha1b cytoplasmic domain."
RN [4]
RP SEQUENCE FROM N.A.
RA MEDLINE=20284952; PubMed=10826701;
RT Hattori A., Seki N., Hayashi A., Kozuma S., Saito T.;
RL "Genomic structure of mouse and human genes for DNA-PKcs interacting
protein (KIP)."
RN [5]
RP SEQUENCE FROM N.A.
RA TISSUE=Cervix;
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
RN [6]
RP STRUCTURE BY NMR OF 9-191;
RX MEDLINE=20283154; PubMed=10822252;
RA Hwang P.M., Vogel H.J.;
RL "Structures of the platelet calcium- and integrin-binding protein and
the alpha1b-integrin cytoplasmic domain suggest a mechanism for
calcium-regulated recognition; homology modelling and NMR studies."
J. Mol. Recognit. 13:83-92(2000).
CC -!- FUNCTION: MAY CONVERT THE INACTIVE CONFORMATION OF INTEGRIN ALPHA-

Fri Jan 17 13:03:43 2003

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CC IIB/BETA3 TO AN ACTIVE FORM THROUGH THE BINDING TO THE INTEGRIN
CC CYTOPLASMIC DOMAIN.
CC -!- SUBUNIT: INTERACTS WITH THE HETERODIMERIC INTEGRIN ALPHA-
CC IIB/BETA3. INTERACTS WITH THE PROTEIN KINASES SNK AND WITH THE
CC REGION IMMEDIATELY UPSTREAM OF THE KINASE DOMAIN OF DNA-PK.
CC -!- TISSUE SPECIFICITY: UBIQUITOUS.
CC -!- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
CC -----
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CC -----
CC EMBL; U83236; AAB39758.1; -
CC EMBL; U85611; AAB53387.1; -
CC EMBL; U82226; AAC51106.1; -
CC EMBL; AB021866; BAA36281.1; -
CC EMBL; BC000846; AAH00846.1; -
CC PDB; 1DGV; 08-DEC-99.
CC Genew; HGNC:16920; CIB1.
CC MIM; 602293; -
CC InterPro; IPR002048; EF-hand.
CC Pfam; PF00036; efhand; 2.
CC ProDom; PD000012; EF-hand; 1.
CC SMART; SM00054; EFh; 2.
CC PROSITE; PS00018; EF_HAND; 2.
CC Calcium-binding; Repeat; 3D-structure.
CC CA_BIND 116 127 EF-HAND 1 (POTENTIAL).
CC CA_BIND 161 172 EF-HAND 2 (POTENTIAL).
CC CA_BIND 44 44 T -> S (IN REF. 3 AND 5).
CC CONFLICT 44 44
CC SEQUENCE 191 AA; 21717 MW; 9AA6EA7897881E55 CRC64;
CC -----
Query Match 100.0%; Score 957; DB 1; Length 191;
Best Local Similarity 99.5%; Pred. No. 4.1e-69;
Matches 190; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGGSGRSLSKELLAEQDFTLTKEILLAHRRFCELLPQEORTVLESSLRAQVPEQILS 60
Db 1 MGGSGRSLSKELLAEQDFTLTKEILLAHRRFCELLPQEORTVLESSLRAQVPEQILS 60
QY 61 LPELKANPFKERICRVFTSTPAKDSLSFEDFLDLSVFSDTATPDIKSHYAFRIEDFDD 120
Db 61 LPELKANPFKERICRVFTSTPAKDSLSFEDFLDLSVFSDTATPDIKSHYAFRIEDFDD 120
QY 121 GTLNRELSRLVNLCTGEGEDTRLSASEMKQLIDNILEESDIDRDGTINLSEFQHVISR 180
Db 121 GTLNRELSRLVNLCTGEGEDTRLSASEMKQLIDNILEESDIDRDGTINLSEFQHVISR 180
QY 181 PDFASSFKIVL 191
Db 181 PDFASSFKIVL 191
RESULT 2
KIPL_MOUSE STANDARD; PRT; 191 AA.
AC KIPL_MOUSE
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Calcium and integrin-binding protein 1 (Calmyrin) (DNA-PKCS
DE interacting protein) (Kinase interacting protein) (KIP) (CIB).
GN CIB1 OR PRKDCIP OR KIP OR CIB.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Kidney;
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RX MEDLINE=99069785; PubMed=9852683;
RA Seki N., Hayashi A., Abe M., Araki R., Fujimori A., Fukumura R.,
RA Hattori A., Kozuma S., Ohhira M., Hori T., Saito T.;
RT "Chromosomal assignment of the gene for human DNA-PKcs interacting
RT protein (KIP) on chromosome 15q25.3-q26.1 by somatic hybrid analysis
RT and fluorescence in situ hybridization.";
RL J. Hum. Genet. 43:275-277(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Fetal kidney;
RX MEDLINE=99160477; PubMed=10051332;
RA Saito T., Seki N., Hattori A., Hayashi A., Abe M., Araki R.,
RA Fujimori A., Fukumura R., Kozuma S., Matsuda Y.;
RT "Structure, expression profile, and chromosomal location of a mouse
RT gene homologous to human DNA-PKcs interacting protein (KIP) gene.";
RL Mamm. Genome 10:315-317(1999).
RN [3]
RP SEQUENCE FROM N.A.
RC Naik M.U., Naik U.P.;
RA "Cloning and tissue distribution of murine calcium and integrin
RA binding protein, CIB.";
RT Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
RL [4]
RN SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gliss C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald C., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
CC -!- FUNCTION: MAY CONVERT THE INACTIVE CONFORMATION OF INTEGRIN ALPHA-
CC IIB/BETA3 TO AN ACTIVE FORM THROUGH THE BINDING TO THE INTEGRIN
CC CYTOPLASMIC DOMAIN (BY SIMILARITY).
CC -!- SUBUNIT: INTERACTS WITH THE HETERODIMERIC INTEGRIN ALPHA-
CC IIB/BETA3. INTERACTS WITH THE PROTEIN KINASES SNK AND WITH THE
CC REGION IMMEDIATELY UPSTREAM OF THE KINASE DOMAIN OF DNA-PK (BY
CC SIMILARITY).
CC -!- TISSUE SPECIFICITY: UBIQUITOUS.
CC -!- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
CC -----
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CC -----
CC EMBL; AB006463; BAA74429.1; -
CC EMBL; AB017361; BAA36165.1; -
CC EMBL; AF173010; AAG38960.1; -
CC EMBL; AK010345; BAB26868.1; -
CC HSSP; Q99828; 1DGV.
CC MGD; MGI:1344418; Cibl.
CC InterPro; IPR002048; EF-hand.
CC Pfam; PF00036; efhand; 2.
CC ProDom; PD000012; EF-hand; 1.
DR
```

DR SMART; SM00054; EFh; 2.
 DR PROSITE; PS00018; EF_HAND; 2.
 KW Calcium-binding; Repeat.
 FT CA_BIND 116 127 EF_HAND 1 (POTENTIAL).
 FT CA_BIND 161 172 EF_HAND 2 (POTENTIAL).
 SQ SEQUENCE 191 AA; 21763 MW; C85B603A19F9D9AC CRC64;

Query Match 94.5%; Score 904; DB 1; Length 191;
 Best Local Similarity 93.7%; Pred. No. 6.4e-65;
 Matches 179; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 1 MGGSGSRLSKELLAAYQDLTFLETKQELLAHRRFCCLLPQEQRTVESSLRAQVPFEQILS 60
 Db 1 MGGSGSRLSKELLAAYQDLTFLETKQELLAHRRFCCLLPQEQRTVESSLRAQVPFEQILS 60
 QY 61 LPELKANPFEKERICRVFSTSPAKDSLSFEDFLDLVSFSDTATPDIKSHYAFRIFFDDDD 120
 Db 61 LPELKANPFEKERICRVFSTSPAKDSLSFEDFLDLVSFSDTATPDIKSHYAFRIFFDDDD 120
 QY 121 GTLNREXLSRLVNCITGEGEDTRLASASEMKOLIDNILEESDIDRDGTINLSEFQHYISRS 180
 Db 121 GTLDREDSLQVLNCLTGEEDTRLASASEMKOLIDNILEESDIDRDGTINLSEFQHYISRS 180
 QY 181 PDFASSFKIVL 191
 Db 181 PDFASSFKIVL 191

RESULT 3

KIP1_RAT
 ID KIP1_RAT STANDARD; PRT; 191 AA.
 AC Q9R010;

DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Calcium and Integrin-binding protein 1 (Calmyrin) (DNA-PKcs
 DE Interacting protein) (Kinase Interacting protein) (KIP) (CIB).
 GN CIB1 OR PRKDCIP OR KIP OR CIB.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;

RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE-99452760; PubMed-10523297;
 RA Kauselmann G., Weller M., Wulff P., Jessberger S., Konietzko U.,
 RA Scafield J., Staubl U., Bereliter-Hahn J., Streibhardt K., Kuhl D.,
 RT "The polo-like protein kinases Fnk and Snk associate with a Ca(2+)-and
 RT integrin-binding protein and are regulated dynamically with synaptic
 RT plasticity."
 RL EMBO J. 18:5528-5539(1999).

CC -1- FUNCTION: MAY CONVERT THE INACTIVE CONFORMATION OF INTEGRIN ALPHA-
 CC IIB/BETA3 TO AN ACTIVE FORM THROUGH THE BINDING TO THE INTEGRIN
 CC CYTOPLASMIC DOMAIN (BY SIMILARITY).
 CC -1- SUBUNIT: INTERACTS WITH THE HETERODIMERIC INTEGRIN ALPHA-
 CC IIB/BETA3. INTERACTS WITH THE PROTEIN KINASES SNK AND WITH THE
 CC REGION IMMEDIATELY UPSTREAM OF THE KINASE DOMAIN OF DNA-PK (BY
 CC SIMILARITY).
 CC -1- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.

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DR EMBL; AF136585; AAF08368.1; -
 DR HSSP; Q99828; IDGV.
 DR InterPro; IPR002048; EF-hand.
 DR Pfam; PF00036; ehand; 2.
 DR ProDom; PD000012; EF-hand; 1.

DR SMART; SM00054; EFh; 2.
 DR PROSITE; PS00018; EF_HAND; 2.
 KW Calcium-binding; Repeat.
 FT CA_BIND 116 127 EF_HAND 1 (POTENTIAL).
 FT CA_BIND 161 172 EF_HAND 2 (POTENTIAL).
 SQ SEQUENCE 191 AA; 21800 MW; 3B00E0228879FCC7 CRC64;

Query Match 94.4%; Score 903; DB 1; Length 191;
 Best Local Similarity 93.7%; Pred. No. 7.7e-65;
 Matches 179; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 MGGSGSRLSKELLAAYQDLTFLETKQELLAHRRFCCLLPQEQRTVESSLRAQVPFEQILS 60
 Db 1 MGGSGSRLSKELLAAYQDLTFLETKQELLAHRRFCCLLPQEQRTVESSLRAQVPFEQILS 60
 QY 61 LPELKANPFEKERICRVFSTSPAKDSLSFEDFLDLVSFSDTATPDIKSHYAFRIFFDDDD 120
 Db 61 LPELKANPFEKERICRVFSTSPAKDSLSFEDFLDLVSFSDTATPDIKSHYAFRIFFDDDD 120
 QY 121 GTLNREXLSRLVNCITGEGEDTRLASASEMKOLIDNILEESDIDRDGTINLSEFQHYISRS 180
 Db 121 GTLDREDSLQVLNCLTGEEDTRLASASEMKOLIDNILEESDIDRDGTINLSEFQHYISRS 180
 QY 181 PDFASSFKIVL 191
 Db 181 PDFASSFKIVL 191

RESULT 4

KIP2_MOUSE
 ID KIP2_MOUSE STANDARD; PRT; 187 AA.
 AC Q9Z309;

DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Kinase Interacting protein 2 (KIP 2).
 GN KIP2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;

RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain, and Testis;
 RX MEDLINE-99132027; PubMed-9931475;
 RA Seki N., Hattori A., Hayashi A., Kozuma S., Ohlra M., Horl T.,
 RA Saito T.,
 RT "Structure, expression profile and chromosomal location of an isoolog
 RT of DNA-PKcs interacting protein (KIP) gene."
 RL Blochim. Biophys. Acta 1444:143-147(1999).

CC -1- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
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DR EMBL; AB016080; BAA36545.1; -
 DR HSSP; Q99828; IDGV.
 DR MGD; MGI:1929293; KIP2.
 DR InterPro; IPR002048; EF-hand.
 DR Pfam; PF00036; ehand; 3.
 DR ProDom; PD000012; EF-hand; 1.
 DR SMART; SM00054; EFh; 2.
 DR PROSITE; PS00018; EF_HAND; 2.
 DR Calcium-binding; Repeat.
 FT CA_BIND 116 127 EF_HAND 1 (POTENTIAL).
 FT CA_BIND 157 168 EF_HAND 2 (POTENTIAL).
 SQ SEQUENCE 187 AA; 21703 MW; D21D21DCBD0B6F5C CRC64;

DB	I MGNRQIIFILFELQEDRIQDIPFIRNRE	
QY	57 QILSLPELKANPFKERICRVFSTSPAKDSLSFEFDLLSVFSDTATPDIKSHYAFRIFD	116
Db	58 LIIQMPELRENPFKERIVAAPS-EDGEGNLTENDFVDMFSVLCEAPRELKANYAFKIYD	116
QY	117 FDDDGTLNREXLSRLVNCLTGEGETRLSASEMKQLIDNIILEESDIDRDGTINLSEFHV	176
Db	117 FNTDNFICKEDLELTLARLT----KSELDEEEVVLCVKVIEEADLDGDKLGCFADFEM	172
QY	177 ISRSPDFASSFKI	189
Db	173 IAKAPDFLSTFHI	185

RESULT 6	CALB_NAEGR	STANDARD;	PRT;	177 AA.
ID	CALB_NAEGR	STANDARD;	PRT;	177 AA.
AC	P42322;			
DT	01-NOV-1995 (Rel. 32, Created)			
DT	01-NOV-1995 (Rel. 32, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Calcineurin B subunit (Protein phosphatase 2B regulatory subunit)			
DE	(Calcineurin regulatory subunit).			
GN	CNBI.			
OS	Naegleria gruberi.			
OC	Eukaryota; Heterolobosea; Schizopyrenida; Vahlkampfiidae; Naegleria.			
OX	NCBI_TaxID=5762;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=NEG;			
RX	MEDLINE=95172399; PubMed=7867946;			
RA	Remillard S.P., Lai E.Y., Levy Y.Y., Fulton C.;			
RA	"A calcineurin-B-encoding gene expressed during differentiation of			
RT	the amoebflagellate Naegleria gruberi contains two introns."			
RL	Gene 154:39-45(1995).			
CC	- - FUNCTION: REGULATORY SUBUNIT OF CALCINEURIM, A CALCIUM-DEPENDENT,			
CC	CALMODULIN STIMULATED PROTEIN PHOSPHATASE. CONFERS CALCIUM			
CC	SENSITIVITY (BY SIMILARITY).			
CC	- - SUBUNIT: COMPOSED OF A CATALYTIC SUBUNIT (A) AND A REGULATORY			
CC	SUBUNIT (B) (BY SIMILARITY).			
CC	- - MISCELLANEOUS: THIS PROTEIN HAS FOUR FUNCTIONAL CALCIUM-BINDING			
CC	SITES (BY SIMILARITY).			
CC	- - SIMILARITY: CONTAINS 4 EF-HAND CALCIUM-BINDING DOMAINS.			
CC	-----			
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CC	-----			
CC	EMBL; U04380; AAA81896.1; -.			
DR	HSSP; P06705; 1AU1.			
DR	InterPro; IPR002048; EF-hand.			
DR	Pfam; PF00036; ehand; 4.			
DR	ProDom; PD000012; EF-hand; 2.			
DR	SMART; SM00054; EFh; 4.			
DR	PROSITE; PS00018; EF_HAND; 4.			
KW	Calcium-binding; Repeat.			
FT	CA_BIND 38 49			EF-HAND 1 (BY SIMILARITY).
FT	CA_BIND 70 81			EF-HAND 2 (BY SIMILARITY).
FT	CA_BIND 107 118			EF-HAND 3 (BY SIMILARITY).
FT	CA_BIND 148 159			EF-HAND 4 (BY SIMILARITY).
SQ	SEQUENCE 177 AA; 20057 MW; 01D4A48E6947E97C CRC64;			
Query Match	22.5%;	Score	215.5;	DB 1; Length 177;
Best Local Similarity	29.2%;	Pred. No.	1.8e-10;	
Matches	52; Conservative	40; Mismatches	73; Indels	13; Gaps 3;
QY	1 MGGSGRLSKELLAAYQDLTLTKQELLAHRRFCCELLPQEQRTVSSLRAQVFEILS 60			

[illegible]


```
Db 1 MGNTSSLRPEEVEEMOKGTNFTQKEIKLYKRFKKLDKDGNGTISK-----DEFLM 52
QY 61 LPELKANPEKERICRVFSTSPAKDSLSEFEDFLDLLSVFSDTATPDIKSHYAFRIFFDDDD 120
Db 53 IPELAVNPVLKRVISIFDEN-GDGSVNFKEFIALSVFNAOGDKOKRLEFAFKYDIDGD 111
QY 121 GTLNREXLSRLVNCLTGEGEDTRLASSEMQLIDNILEESDIDRGTINLSEFOHVIS 178
Db 112 GYISNGELFTVLKMMVG-----NNISDVQLQOIVDKTILEADEDDGDKISFEFEAKTIS 165

, RESULT 7
CALB_SCHPO STANDARD; PRT; 174 AA.
AC Q9U93;
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Calcineurin B subunit (Protein phosphatase 2B regulatory subunit)
DE (Calcineurin regulatory subunit).
GN CNB1 OR SPC830.06.
OS Schizosaccharomyces pombe (fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volkert G., Aert R., Robben J., Grymoprez B.,
RA Weltjens I., Vansteelt E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritz C., Holzer E., Moesti D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gallardin C., Tallada V.A., Garzon A., Thode G.,
RA Dominguez A., Revuelta J.L., Moreno S., Sanchez M., del Rey F., Benito J.,
RA Cerrutti L., Lowe T., McComble W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe.";
RL Nature 415:871-880(2002).
CC -1- FUNCTION: REGULATORY SUBUNIT OF CALCINEURIN, A CALCIUM-DEPENDENT,
CC CALMODULIN STIMULATED PROTEIN PHOSPHATASE. CONFERS CALCIUM
CC SENSITIVITY (BY SIMILARITY).
CC -1- SUBUNIT: COMPOSED OF A CATALYTIC SUBUNIT (A) AND A REGULATORY
CC SUBUNIT (B) (BY SIMILARITY).
CC RT MISCELLANEOUS: THIS PROTEIN HAS FOUR FUNCTIONAL CALCIUM-BINDING
CC SITES (BY SIMILARITY).
CC RL -1- SIMILARITY: CONTAINS 4 EF-HAND CALCIUM-BINDING DOMAINS:
CC -----
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DR EMBL; AL109850; CAB52879.1; -.
DR HSSP; P06705; 1AUI.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR001125; Recoverin.
DR Pfam; PF00036; ehnd; 4.
DR PRINTS; PR00450; RECOVERIN.
DR ProDom; PD000012; EF-hand; 1.
DR SMART; SM00054; EFh; 4.
DR PROSITE; PS00018; EF_HAND; 4.
KW Calcium-binding; Myristate.
FT CA_BIND 34 45 EF-HAND 1 (BY SIMILARITY).
FT CA_BIND 66 77 EF-HAND 2 (BY SIMILARITY).
FT CA_BIND 103 114 EF-HAND 3 (BY SIMILARITY).
FT CA_BIND 144 155 EF-HAND 4 (BY SIMILARITY).
SQ SEQUENCE 174 AA; 19675 MW; EEF38FE74959442E.CRC64;

Query Match 21.9%; Score 209.5; DB 1; Length 174;
Best Local Similarity 27.2%; Pred. No. 5.2e-10;
Matches 49; Conservative 46; Mismatches 68; Indels 17; Gaps 4;

QY 1 MGSGSRSLKELLAEYQDLTFLTKQELLAHRFCELLPQEQRTVESSLRAQVPEQILS 60
Db 1 MGSGSQIFEDLISN---SFSNEIERIKRFRK-----IDANQGSIDRNEFLS 48
QY 61 LPELKANPEKERICRVFSTSPAKDSLSEFEDFLDLLSVFSDTATPDIKSHYAFRIFFDDDD 120
Db 49 IPSVANSPLASRLFSVDEDDGGD-VDFQEFINSLSVFSVHGKKEKLFKFAFKYDIDRD 107
QY 121 GTLNREXLSRLVNCLTGEGEDTRLASSEMQLIDNILEESDIDRGTINLSEFOHVISRS 180
Db 108 GYISNGELFTVLKMMVG-----TNLRDQLQOIVDKTMEYDKDRDGKISFEFEKDIYVSGS 163

RESULT 8
CALB_NEUCR STANDARD; PRT; 174 AA.
AC P87072; O13408;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Calcineurin B subunit (Protein phosphatase 2B regulatory subunit)
DE (Calcineurin regulatory subunit).
GN CNB-1 OR CAN-B.
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=74A;
RX MEDLINE=98007857; PubMed=9349701;
RA Prokisch H., Yarden O., Dieminger M., Tropschug M., Barthelmess I.B.;
RT "Impairment of calcineurin function in Neurospora crassa reveals its
RT essential role in hyphal growth, morphology and maintenance of the
RT apical Ca2+ gradient.";
RL Mol. Gen. Genet. 256:104-114(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=98345933; PubMed=9680955;
RA Kothe G.O., Free S.J.;
RT "Calcineurin subunit B is required for normal vegetative growth in
RT Neurospora crassa.";
RL Fungal Genet. Biol. 23:248-258(1998).
CC -1- FUNCTION: REGULATORY SUBUNIT OF CALCINEURIN, A CALCIUM-DEPENDENT,
CC CALMODULIN STIMULATED PROTEIN PHOSPHATASE. CONFERS CALCIUM
CC SENSITIVITY.
CC -1- SUBUNIT: COMPOSED OF A CATALYTIC SUBUNIT (A) AND A REGULATORY
CC SUBUNIT (B).
CC RT MISCELLANEOUS: THIS PROTEIN HAS FOUR FUNCTIONAL CALCIUM-BINDING
CC SITES.
CC RL -1- SIMILARITY: CONTAINS 4 EF-HAND CALCIUM-BINDING DOMAINS.
CC -----
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Db 1 GAAPSKIVDGLLED---TNFDRDEIERLRKRKRMKLDRSSGSIDKN-----EFMSI 48
QY 62 PELKANPFKERICRVFSTSPAKDSLSFEDFLDLLSVFSDTATPDIKSHYAFRIPDFDDG 121
Db 49 PGVSSNPLAGRIMEVFADNSGD-VDFQEFITGLSIFSGRGSKDEKLRFAFKIYDIDKDG 107
QY 122 TLNREXLSRLVNCLTGEGEDTRLASASEMKQILIDNILEESDIDRDGTINLSEFOHYI 177
Db 108 FISNGELFIVLKIMVG---SNLDDEQLQOIIVDRITVENSDSDGRLSFEEFKNAI 159

RESULT 10
CALB_HUMAN
ID CALB_HUMAN STANDARD; PRT; 169 AA.
AC P06705; P15117; Q08044;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Calcineurin B subunit isoform 1 (Protein phosphatase 2B regulatory subunit 1) (Protein phosphatase 3 regulatory subunit B alpha isoform 1).
GN PPP3R1 OR CNB OR CNA2.
OS Homo sapiens (Human),
OS Bos taurus (Bovine), and
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606, 9913, 10116;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=Human;
RX MEDLINE=90126237; PubMed=2558868;
RA Guerini D., Krinks M.H., Sikela J.M., Hahn W.E., Klee C.B.;
RT "Isolation and sequence of a cDNA clone for human calcineurin B, the
RT Ca2+-binding subunit of the Ca2+/calmodulin-stimulated protein
RT phosphatase.";
RL DNA 8:675-682(1989).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=Bovine;
RA Nargang C.E., Bottorff D.A., Adachi K.;
RL Submitted (APR-1993) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 1-168.
RC SPECIES=Bovine; TISSUE=Brain;
RX MEDLINE=84132092; PubMed=6321184;
RA Altken A., Klee C.B., Cohen P.;
RT "The structure of the B subunit of calcineurin.";
RL Eur. J. Biochem. 139:663-671(1984).
RN [4]
RP SEQUENCE FROM N.A.
RC SPECIES=Rat;
RA Perrino B.A., Huang X., Ng L.Y., Soderling T.R.;
RL Submitted (xxx-1992) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RC SPECIES=Rat; TISSUE=Brain, and Testis;
RX MEDLINE=94153993; PubMed=8110831;
RA Chang C.-D., Mukai H., Kuno T., Tanaka C.;
RT "cDNA cloning of an alternatively spliced isoform of the regulatory subunit of Ca2+/calmodulin-dependent protein phosphatase (calcineurin B alpha 2)."
RL Biochim. Biophys. Acta 1217:174-180(1994).
RN [6]
RP CALCIUM-BINDING DATA.
RC SPECIES=Bovine;
RX MEDLINE=80101597; PubMed=293720;
RA Klee C.B., Crouch T.H., Krinks M.H.;
RT "Calcineurin: a calcium- and calmodulin-binding protein of the
RT nervous system.";
RL Proc. Natl. Acad. Sci. U.S.A. 76:6270-6273(1979).
RN [7]
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).

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RC SPECIES-Bovine; MEDLINE=95360994; PubMed=75433369;
RX Griffith J.P., Kim J.L., Kim E.E., Shtuchak M.D., Thomson J.A.,
RA Fitzgibbon M.J., Fleming M.A., Caron P.R., Hsiao K., Navia M.A.;
RT "X-ray structure of calcineurin inhibited by the immunophilin-
RL Immunosuppressant FKBP12-FK506 complex.";
RN Cell 82:507-522(1995).
RP [8]
RX X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
RC SPECIES-Human;
RX MEDLINE=96097077; PubMed=8524402;
RA Kissinger C.R., Parge H.E., Knighton D.R., Lewis C.T., Pelletier L.A.,
RA Tempczyk A., Kalish V.J., Tucker K.D., Showalter R.E., Moornaw F.W.,
RA Gastinel L.N., Habuka N., Chen X., Maldonado F., Barker J.E.,
RA Bacquet R., Villafranca J.E.;
RT "Crystal structures of human calcineurin and the human FKBP12-FK506-
RL calcineurin complex.";
RX Nature 378:641-644(1995).
CC -1- FUNCTION: REGULATORY SUBUNIT OF CALCINEURIN, A CALCIUM-DEPENDENT,
CC CALMODULIN STIMULATED PROTEIN PHOSPHATASE. CONFERS CALCIUM
CC SENSITIVITY.
CC -1- SUBUNIT: COMPOSED OF A CATALYTIC SUBUNIT (A) AND A REGULATORY
CC SUBUNIT (B).
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND 2; ARE
CC PRODUCED BY ALTERNATIVE SPLICING IN RAT.
CC -1- TISSUE SPECIFICITY: ISOFORM 2 IS TESTIS-SPECIFIC.
CC -1- MISCELLANEOUS: THIS PROTEIN HAS FOUR FUNCTIONAL CALCIUM-BINDING
CC SITES.
CC -1- SIMILARITY: CONTAINS 4 EF-HAND CALCIUM-BINDING DOMAINS.
-----
DR EMBL; M30773; AAB08721.1; -
DR EMBL; X71666; CA50659.1; -
DR EMBL; L03554; AAA40854.1; -
DR EMBL; D14568; BAA03422.1; -
DR EMBL; D14425; BAA03318.1; -
DR PIR; A33391; A33391.
DR PIR; S34127; S34127.
DR PIR; JT0297; JT0297.
DR PIR; S42716; S42716.
DR PIR; S42717; S42717.
DR PDB; 1AUT; 03-DEC-97.
DR PDB; 1TCO; 12-FEB-97.
DR Genew; HGNC:9317; PPP3R1.
DR MIM; 601302; -
DR InterPro; IPR002048; EF-hand.
DR Pfam; PF00036; ehand; 4.
DR ProDom; PDO00012; EF-hand; 2.
DR SMART; SMO0054; EFh; 4.
DR PROSITE; PS00018; EF_HAND; 4.
KW Calcium-binding; Repeat; Alternative splicing; Myristate;
KW 3D-structure.
FT INIT_MET 0
FT LIPID 1 MYRISTATE.
FT CA_BIND 30 EF-HAND 1.
FT CA_BIND 62 EF-HAND 1.
FT CA_BIND 99 EF-HAND 2.
FT CA_BIND 140 EF-HAND 3.
FT CA_BIND 151 EF-HAND 4.
FT VARSPIC 1 G->MEQGTDIQSQIFPPTERKNFWKKGDKDFRONKYPSFR
FT CONFLICT 11 ELYNLIFFADRKQ (IN ISOFORM 2).
FT CONFLICT 153 C->M (IN REF. 3).
FT SEQUENCE 169 AA; 19169 MW; 749141BD0434C90C CRC64;
Query Match 19.4%; Score 185.5; DB 1; Length 169;
Best Local Similarity 31.18; Pred. No. 4e-08;

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RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirska R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of *Drosophila melanogaster*,"
RL Science 287:2185-2195(2000).
CC -I- FUNCTION: CALCINEURIN IS A CALCIUM BINDING AND CALMODULIN BINDING
CC PROTEIN FOUND IN ALL CELLS FROM YEAST TO MAMMALS, IT IS A CALCIUM
CC DEPENDENT, CALMODULIN STIMULATED PROTEIN PHOSPHATASE (BY
CC SIMILARITY).
CC -I- SUBUNIT: COMPOSED OF TWO COMPONENTS (A AND B), THE A COMPONENT IS
CC THE CATALYTIC SUBUNIT AND THE B COMPONENT CONFERES CALCIUM
CC SENSITIVITY (BY SIMILARITY*).
CC -I- MISCELLANEOUS: THIS PROTEIN HAS FOUR FUNCTIONAL CALCIUM-BINDING
CC SITES.
CC -I- SIMILARITY: TO OTHER EF-HAND CALCIUM BINDING PROTEINS.
CC -I- CAUTION: Ref.2 sequence differs from that shown due to erroneous
CC gene model prediction.
CC -----
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CC -----
DR EMBL; U56245; AAC47350.1; -
DR EMBL; AE003840; AAF59195.1; ALT_SEQ.
DR HSSP; P06705; 1TCO.
DR FlyBase; FBgn0015614; Canb2.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR001125; Recoverin.
DR Pfam; PF00036; efhand; 4.
DR PRINTS; PR00450; RECOVERIN.
DR ProDom; PD000012; EF-hand; 2.
DR SMART; SM00054; Efh; 4.
DR PROSITE; PS00018; EF_HAND; 4.
KW Calcium-binding; Repeat.
FT CA_BIND 31 42 EF_HAND 1 (POTENTIAL).
FT CA_BIND 63 74 EF_HAND 2 (POTENTIAL).
FT CA_BIND 100 111 EF_HAND 3 (POTENTIAL).
FT CA_BIND 141 152 EF_HAND 4 (POTENTIAL).
SQ SEQUENCE 170 AA; 19267 MW; FDB1BD9DB5A4BDEC CRC64;

Query Match 18.5%; Score 177.5; DB 1; Length 170;
Best Local Similarity 24.7%; Pred. No. 1.7e-07;
Matches 44; Conservative 43; Mismatches 72; Indels 19; Gaps 4;

QY 3 GSGSRLSKELLAEYQDLTLTKQELLAHRRCELLPQEQRTVESLSRAQVFEQILSLP 62
Db 2 GNETSIPMCMCSNFD-----ADEIRRLGKR-----RKLDLNSGALSVDSEMSLP 47

QY 63 ELKANPFRERICRVSTSPAKDSLSEFEDLLSVSDTATPDIKSHYAFRIEDDDGT 122
Db 48 ELQONPLVQRAVIDIFD-ADGNGEVDKFEFIQGVSVKSKLRLRAFRIRYDMNDGY 106

QY 123 LNRXLSRLVNCLTGEGEDTRLSASEMKOLIDNILESDIDRDGTINSEFQHVISRS 180
Db 107 ISNGELFOYLKMMVG---NNLKDTQLQOIVDKTIGFADKDEDEKISDFEFCSSVVGNT 160

RESULT 13
CA22_MOUSE STANDARD; PRT; 194 AA.
AC Q62877;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Calcium-binding protein p22 (Calcium-binding protein CHP) (Calcineurin

DE homologous protein) (S1d470).
GN CHP.
OS Mus musculus (Mouse), and
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090, 10116;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES-Rat; TISSUE-Liver;
RX MEDLINE=96215311; PubMed=8626580;
RA Barroso M.R., Bernd K.K., Dewitt N.D., Chang A., Mills K.,
RA Szul E.S.;
RT "A novel Ca2+-binding protein, p22, is required for constitutive
RT membrane traffic.";
RL J. Biol. Chem. 271:10183-10187(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES-Rat; TISSUE-Brain;
RX MEDLINE=21374135; PubMed=11481038;
RA Matsumoto M., Miyake Y., Nagita M., Inoue H., Shitakubo D.,
RA Takemoto K., Ohtsuka C., Murakami H., Nakamura N., Kanazawa H.;
RT "A serine/threonine kinase which causes apoptosis-like cell death
RT interacts with a calcineurin B-like protein capable of binding Na+/H+
RT exchanger.";
RL J. Biochem. 130:217-225(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES-Mouse;
RA Seki N., Hattori A., Hayashi A., Kozuma S., Muramatsu M., Saito T.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC SPECIES-Mouse; STRAIN-C57BL/6J; TISSUE-Liver;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staahl F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carlinici P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weltz C., Wittaker C., Wilming L.,
RA Wyszynski-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [1]
RP FUNCTION: REQUIRED FOR CONSTITUTIVE MEMBRANE TRAFFIC.
CC -I- SUBCELLULAR LOCATION: Cytoplasmic.
CC -I- TISSUE SPECIFICITY: UBICITOUSLY EXPRESSED.
CC -I- PTM: BOTH N-MYRISTOYLATION AND CALCIUM-MEDIATED CONFORMATIONAL
CC CHANGES ARE ESSENTIAL FOR ITS FUNCTION.
CC -I- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
CC -----
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CC -----
DR EMBL; U39875; AAB04146.1; -
DR EMBL; AB070350; BAB63369.1; -
DR EMBL; AB025217; BAA84688.1; -

QY 86 LSFEDFLDLVSFSDTATPDIKSHYAFRFDDEDDGTLNREXLSRLVNCITGEGEDTRL 145
 Db 70 VDKREFIQGVQSFSVRGDKLSKLRFAFRITYDMNDGYISNGELFQVLKMMVG----NLK 125
 QY 146 ASEMQLIDNILEESDIDRDGTINLSEFQHVISR 180
 Db 126 DTQLQOIVDKTICFADKDEGKISFDEFCVVGNT 160

RESULT 15
 CA22_HUMAN
 ID CA22_HUMAN STANDARD: PRT; 194 AA.
 AC Q99653;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Calcium-binding protein p22 (Calcium-binding protein CHP) (Calcineurin homologous protein) (Calcineurin B homolog).
 GN CHP.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-B-cell;
 RX MEDLINE=97057295; PubMed=8901634;
 RA Lin X., Barber D.L.;
 RT "A calcineurin homologous protein inhibits GTPase-stimulated Na-H exchange."
 RL Proc. Natl. Acad. Sci. U.S.A. 93:12631-12636(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Muscle;
 RA Strausberg R.;
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: REQUIRED FOR CONSTITUTIVE MEMBRANE TRAFFIC (BY SIMILARITY). INHIBITS GTPASE-STIMULATED NA-H EXCHANGE. SPECIFICALLY BINDS TO THE SODIUM/HYDROGEN EXCHANGER 1 (NHE1) AT A DOMAIN THAT IS CRITICAL FOR GROWTH FACTOR STIMULATION OF EXCHANGE ACTIVITY.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- TISSUE SPECIFICITY: UBIQUITOUSLY EXPRESSED. HAS BEEN FOUND IN FETAL EYE, LUNG, LIVER, MUSCLE, HEART, KIDNEY, THYMUS AND SPLEEN.
 CC -1- PTM: BOTH N-MYRISTOYLATION AND CALCIUM-MEDIATED CONFORMATIONAL CHANGES ARE ESSENTIAL FOR ITS FUNCTION IN EXOCYTIC TRAFFIC (BY SIMILARITY).
 CC -1- PTM: PHOSPHORYLATED IN VIVO. DECREASE IN ITS PHOSPHORYLATION IS ASSOCIATED WITH AN INCREASE IN EXCHANGE ACTIVITY. THE PHOSPHORYLATION STATE MAY REGULATE THE BINDING TO NHE1.
 CC -1- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: U61538; AAB37770.1;
 DR EMBL: BC001646; AAH01646.1;
 DR HSSP: P06705; 1AUI.
 DR MIM: 606988;
 DR InterPro: IPR002048; EF-hand.
 DR Pfam: PF00036; efhand; 3.
 DR ProDom: PD000012; EF-hand; 2.
 DR SMART: SM00054; EFh; 2.
 DR PROSITE: PS00018; EF_HAND; FALSE_NEG.
 KW Calcium-binding; Repeat; Myristate; Phosphorylation.
 FT INT_MET 0
 FT LIPID 1
 FT DOMAIN 38 49 MYRISTATE (BY SIMILARITY).
 ANCESTRAL CALCIUM SITE 1 (POTENTIAL).

FT DOMAIN 70 81 ANCESTRAL CALCIUM SITE 2 (POTENTIAL).
 FT CA_BIND 122 133 EF-HAND 3 (BY SIMILARITY).
 FT CA_BIND 163 174 EF-HAND 4 (BY SIMILARITY).
 SQ SEQUENCE 194 AA; 22325 MW; 17DDEE5F03C88380 CRC64;
 Query Match 18.0%; Score 172; DB 1; Length 194;
 Best local similarity 26.3%; Pred. No. 5.6e-07;
 Matches 51; Conservative 35; Mismatches 76; Indels 32; Gaps 6;
 QY 5 GSR---LSKELLAERYQDLFTLTKQETLLAHRFCCELLPQEQRYESSLRAQVPFEQILS 60
 Db 1 GSRASTLLRDELELEIKKETGFSSQITRLYSRFTSLDKGENGLSR-----EDFQR 52
 QY 61 LPELKANPKEKRICRVFSTSPAKDSLSEDFDLDSVF-----SDTATPD----- 105
 Db 53 IPELAINDPLGDRILINAFPE-GEQVAFRGFMRTLAHFRPIEDNEKSKDVNGPEPLNSRS 111
 QY 106 IKSHYAFRIEDFDDGTLNREXLSRLVNCITGEGEDTRLASSEMQLIDNILEESDIDRD 165
 Db 112 NKLHFAFRLLYDLDKDEKISRDELLQVLRMMVG---VNISDQLGSIADRTIQEADQDGD 167
 QY 166 GTINLSEFQHVISR 179
 Db 168 SAISFTFEVVKVLEK 181

Search completed: January 17, 2003, 12:48:33
 Job time : 13 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 17, 2003, 12:42:03 : Search time 35 Seconds
(without alignments)
727.168 Million cell updates/sec

Title: MUT127
Perfect score: 957
Sequence: 1 MCGSGSRLSKELLAELYDLT.....EFQHVISRSPDFASSFKIVL 191

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	951	99.4	191	AAW51215	Amino acid sequenc
2	945	98.7	191	AAW62287	Human protein phos
3	943	98.5	191	AAW64199	Human interferon r
4	372	38.9	172	AAU87324	Novel central nerv
5	372	38.9	184	AAW43562	Human polypeptide
6	370	38.7	185	AAW64418	Amino acid sequenc
7	355	37.1	173	ABB96054	Human testicular a
8	355	37.1	173	AAU87612	Novel central nerv
9	355	37.1	173	AAW95362	Human reproductive
10	355	37.1	173	AAW43637	Human polypeptide

11	355	37.1	173	22	AAU19952	Novel human calcit
12	338	35.3	187	22	AAE09736	Human kinase inter
13	337.5	35.3	206	22	ABB64325	Drosophila melanog
14	237.5	24.8	169	23	ABP41194	Human ovarian anti
15	220	23.0	120	20	AAU11976	Human 5' EST secre
16	201.5	21.1	175	20	AAU00881	Calcineurin regula
17	188	19.6	175	21	AAU21178	Zea mays protein f
18	188	19.6	210	21	AAU21177	Zea mays protein f
19	187	19.5	175	21	AAU51586	Arabidopsis thalia
20	187	19.5	175	23	ABB92357	Herbicidally activ
21	185	19.3	175	21	AAU07824	Arabidopsis thalia
22	183.5	19.2	170	19	AAW64200	Human calcineurin.
23	183.5	19.2	170	21	AAU09978	Human HCNB protei
24	179.5	18.8	189	22	ABB58936	Drosophila melanog
25	178	18.6	169	21	AAU51587	Arabidopsis thalia
26	176	18.4	169	21	AAU07825	Arabidopsis thalia
27	174	18.2	187	21	AAU21179	Zea mays protein f
28	173.5	18.1	187	22	ABB61857	Drosophila melanog
29	173.5	18.1	187	22	ABB67063	Drosophila melanog
30	172.5	18.0	162	22	ABB65554	Drosophila melanog
31	171.5	17.9	170	22	ABB60493	Drosophila melanog
32	167	17.5	170	21	AAU09977	Human CNBT protei
33	167	17.5	170	22	AAU14411	Human calcineurin B
34	167	17.5	173	22	AAU64410	Human polypeptide
35	167	17.5	187	22	AAU87327	Novel human calcit
36	167	17.5	189	22	ABB95936	Novel central nerv
37	167	17.5	189	22	AAU87615	Human testicular a
38	167	17.5	189	22	AAU95239	Novel central nerv
39	167	17.5	189	22	AAU43564	Human reproductive
40	167	17.5	189	22	AAU43639	Human polypeptide
41	167	17.5	189	22	AAU19951	Novel human calcit
42	161.5	16.9	226	21	AAU47032	Arabidopsis thalia
43	160.5	16.8	226	21	AAU21763	Arabidopsis thalia
44	154	16.1	190	21	AAU69996	Human receptor-ass
45	153	16.0	194	22	AAU87585	Novel central nerv

ALIGNMENTS

RESULT 1	
AAW51215	
ID	AAW51215 standard; protein; 191 AA.
XX	
AC	AAW51215;
XX	
DT	21-AUG-1998 (first entry)
XX	
DE	Amino acid sequence of the calcium-integrin binding protein.
XX	
KW	Human calcium-integrin binding protein; CIB; Integrin alpha IIB;
KW	cytoplasmic domain; platelet; alpha IIB-beta-3; fibrinogen receptor;
KW	Inhibition; blood coagulation; vascular disorder.
XX	
OS	Homo sapiens.
XX	
FH	Key
FT	Region
FT	Location/Qualifiers
FT	/note- "EF-hand motif"
FT	116..128
FT	160..173
XX	/note- "EF-hand motif"
PN	W09814471-A1.
XX	
PD	09-APR-1998.
XX	
PF	24-SEP-1997; 97W0-US16828.
XX	
PR	02-OCT-1996; 96US-0720625.
XX	
PA	(UYNC-) UNIV NORTH CAROLINA.
XX	
PI	Naik UP, Parise LV;

XX WPI; 1998-240018/21.
DR N-PSDB; AAV07211.
XX
XX New isolated calcium-integrin binding protein - is expressed in
PT platelets and activates the fibrinogen receptor, used to develop
PT products for treating e.g. vascular disorders
XX
XX Claim 1; Page 30; 44pp; English.
XX This is the amino acid sequence of the human calcium-integrin binding
CC (CIB) protein, that binds to the integrin alpha IIB cytoplasmic
GC domain. The CIB protein is expressed in platelets and interacts with
CC the alpha IIB subunit of integrin alpha IIB- beta 3, to activate the
CC fibrinogen receptor. Inhibitory compounds can be used to inhibit the
CC activation of the fibrinogen receptor where it is desired to reduce
CC blood coagulation for therapeutic, diagnostic or pharmaceutical
CC reasons. The products can be used for treating vascular disorders,
CC and for isolating or purifying integrins or fibrinogen. They can also
CC be used for detection and diagnosis.
XX
SQ Sequence 191 AA;
Query Match 99.4%; Score 951; DB 19; Length 191;
Best Local Similarity 99.0%; Pred. No. 2.9e-95;
Matches 189; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 MGGSGSRLSKELLAQYQDLTLTKQEILLAHRRFCELLPQEQRTVLESSLRAQVPFEQILS 60
Db 1 MGGSGSRLSKELLAQYQDLTLTKQEILLAHRRFCELLPQEQRSVLESSLRAQVPFEQILS 60
QY 61 LPELKANPFKERICRVFSTSPAKDSLSFEFLLSLVFSFSDTATPDIKSHYAFRIFDFFF 120
Db 61 LPELKANPFKERICRVFSTSPAKDSLSFEFLLSLVFSFSDTATPDIKSHYAFRIFDFFF 120
QY 121 GTLNREXLSRLVNCLTGEGEDTRLSASEMKQLIDNILESDIDRDGTINLSEFQHVISRS 180
Db 121 GTLNREXLSRLVNCLTGEGEDTRLSASEMKQLIDNILESDIDRDGTINLSEFQHVISRS 180
QY 181 PDFASFSFKIVL 191
Db 181 PDFASFSFKIVL 191
RESULT 2
AAW62287
ID AAW62287 standard; Protein; 191 AA.
XX
AC AAW62287;
XX
XX 24-SEP-1998 (first entry)
XX Human protein phosphatase regulatory subunit.
DE Human; protein phosphatase regulatory subunit; HCNB; diagnosis;
XX immunosuppression; neurodegeneration; inflammation; cancer.
KW Homo sapiens.
OS
XX
FH Key Location/Qualifiers
FT Misc-difference 44 /label= unknown
FT /note= "encoded by ASG"
FT Misc-difference 45 /label= unknown
FT /note= "encoded by TGN"
XX
PN W09826056-A1.
XX
XX 18-JUN-1998.
PD
XX
XX 25-NOV-1997; 97WO-US21603.
XX

PR 12-DEC-1996; 96US-0764563.
XX (INCY-) INCYTE PHARM INC.
PA
XX Goli SK, Hillman JL;
PI
XX WPI; 1998-348518/30.
DR N-PSDB; V398009.
XX
XX New protein phosphatase regulatory sub-unit - useful for diagnosis,
PT prevention and treatment of immuno-suppression, neuro-degeneration,
PT inflammation and cancer
XX
XX Claim 1; Fig 1; 65pp; English.
XX The present sequence is a pure human protein phosphatase regulatory
CC subunit (HCNB). Host cells, comprising a vector containing DNA encoding
CC HCNB, are used to produce recombinant HCNB which is used to treat or
CC prevent immunosuppression or neurological diseases (especially parasitic,
CC bacterial or viral infections, including AIDS; the effects of radio- or
CC chemo-therapy and Alzheimer's disease). Antagonists which bind
CC specifically to HCNB and modulate its activity are used to treat
CC inflammation, cancer, or immunological disorders and allograft rejection
CC (especially anaemia, asthma, systemic lupus erythematosus, myasthenia
CC gravis, diabetes, thyroiditis, ulcerative colitis, osteoporosis and
CC arthritis). Complements of the DNA encoding HCNB are useful as probes
CC and primers for detecting the DNA encoding HCNB by hybridisation or
CC amplification assays, while Ab can be used to detect HCNB by immunoassay,
CC particularly for diagnosis of the specified disorders, including early
CC diagnosis of cancers. The probes can also be used to map the
CC corresponding genomic sequence, while Ab are also useful in drug
CC screening and for purifying native HCNB. Therapeutic agents are
CC administered orally, intravenously, intramuscularly, topically or
CC rectally, normally at 0.1-105 mu g.
XX
SQ Sequence 191 AA;
Query Match 98.7%; Score 945; DB 19; Length 191;
Best Local Similarity 98.4%; Pred. No. 1.3e-94;
Matches 188; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 MGGSGSRLSKELLAQYQDLTLTKQEILLAHRRFCELLPQEQRTVLESSLRAQVPFEQILS 60
Db 1 MGGSGSRLSKELLAQYQDLTLTKQEILLAHRRFCELLPQEQRXESSLRAQVPFEQILS 60
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Db 61 LPELKANPFKERICRVFSTSPAKDSLSFEFLLSLVFSFSDTATPDIKSHYAFRIFDFFF 120
QY 121 GTLNREXLSRLVNCLTGEGEDTRLSASEMKQLIDNILESDIDRDGTINLSEFQHVISRS 180
Db 121 GTLNREXLSRLVNCLTGEGEDTRLSASEMKQLIDNILESDIDRDGTINLSEFQHVISRS 180
QY 181 PDFASFSFKIVL 191
Db 181 PDFASFSFKIVL 191
RESULT 3
AAW64199
ID AAW64199 standard; Protein; 191 AA.
XX
XX AAW64199;
AC
XX
DT 09-NOV-1998 (first entry)
XX Human interferon receptor 1 binding protein IR1B1.
DE Interferon receptor 1 binding protein; IR1B1; human; tumour;
XX cancer; gene therapy; tissue graft; graft survival.
KW
XX
OS Homo sapiens.
XX

PN WO9831796-A1.
XX
PD 23-JUL-1998.
XX
PF 15-JAN-1998; 98WO-US00671.
XX
PR 15-JAN-1997; 97US-0035636.
XX
PA (MCIN/) MCINNIS P A.
XX (YEDA) YEDA RES & DEV CO LTD.
PI Abramovitch C, Chebath JE, Revel M;
DR WPI; 1998-414096/35.
DR N-PSDB; AAV44272.
XX
PT New isolated interferon receptor binding proteins - used to develop
PT products for modulating sensitivity to interferon, e.g. in the
PT treatment of tumours or for prolonging graft survival
XX
PS Claim 1; Page 34; 64pp; English.
XX
CC This is a novel human protein, designated interferon receptor
CC binding protein 1 (IR1B1), which interacts with the intracytoplasmic
CC (IC) domain of the IFNAR1 chain of the interferon type 1 (IFN-alpha,
CC beta or omega) receptor. IR1B1 is a new member of the calcineurin
CC and calcitracin family of calcium-regulated proteins (see also
CC AAW64200). It is induced very rapidly and transiently following IFN
CC treatment of human cells. It was identified in a two-hybrid
CC screening for proteins interacting with the IFNAR1-IC domain;
CC another protein, IR1B4 (see AAW64202), was similarly identified. A
CC cDNA clone (see AAV44272) encoding IR1B1, host cells and expression
CC vectors are claimed. DNA encoding IR1B1 and IR1B4 can be used in
CC cancer therapy where the increased cellular response to IFN would
CC result in a decrease in malignant cell growth and an enhanced
CC response to exogenous IFN therapy. Antisense IR1B1 or IR1B4
CC nucleic acids can be used for prolonging tissue or organ graft
CC survival in patients as the rejection of these grafts in the host
CC is mediated by the histocompatibility antigens (MHC class I) whose
CC synthesis depends on the IFN stimulus. The products can also be
CC used in detection and diagnosis.
XX
SQ Sequence 191 AA;
QY 1 MGGSGSRLSKELAEYQDLTLFTKQEILAHRRFCCLPQEQRTVESSLRAQVPFEQILS 60
DB 1 MGGSGSRLSKELAEYQDLTLFTKQEILAHRRFCCLPQEQRSVSSLRAQVPFEQILS 60
QY 61 LPELKANPFKERICRVSTSPAKDSLSEDFLDLISVSDTATPDIKSHYAFRIFDDDD 120
DB 61 LPELKANPFKERICRVSTSPAKDSLSEDFLDLISVSDTATPDIKSHYAFRIFDDDD 120
QY 121 GTLNREXLSRLVNCJLGEGETRLSASEMKQILIDNILEESDIDRDGTINLSEFQHVISRS 180
DB 121 GTLNREXLSRLVNCJLGEGETRLSASEMKQILIDNILEESDIDRDGTINLSEFQHVISRS 180
QY 181 PDFASSFKIYL 191
DB 181 PDFASSFKIYL 191
RESULT 4
ID AAU87324 standard; Protein; 172 AA.
XX AAU87324;
AC
XX
DT 05-JUN-2002 (first entry)
XX

DE Novel central nervous system protein #234.
XX
KW Central nervous system; CNS; autoimmune disease; rheumatoid arthritis;
KW hyperproliferative disorder; neoplasm; cardiovascular disorder;
KW cardiac arrest; cerebrovascular disorder; ischemia; anglogenesis;
KW nervous system disorder; Alzheimer's disease; AIDS; ocular disorder;
KW acquired immunodeficiency virus; dysphagia; gastrointestinal disorder;
KW adenocarcinoma; reproductive system disorder; testicular feminisation;
KW endocrine disorder; diabetes; cancer; leukaemia; neovascularisation;
KW respiratory disorder; renal disorder; kidney failure; blood disorder;
KW myocardial infarction; wound healing; cell proliferation; skin aging;
KW food additive; food preservative; gene therapy.
XX
OS Homo sapiens.
XX
PN WO200155318-A2.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01332.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226868.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.

PR	14-SEP-2000;	2000US-02323397.
PR	14-SEP-2000;	2000US-02323398.
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PR	14-SEP-2000;	2000US-02324001.
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PR	14-SEP-2000;	2000US-0233064.
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PR	21-SEP-2000;	2000US-0234274.
PR	25-SEP-2000;	2000US-0234997.
PR	25-SEP-2000;	2000US-0234998.
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PR	27-SEP-2000;	2000US-0235836.
PR	29-SEP-2000;	2000US-0236327.
PR	29-SEP-2000;	2000US-0236367.
PR	29-SEP-2000;	2000US-0236368.
PR	29-SEP-2000;	2000US-0236369.
PR	29-SEP-2000;	2000US-0236370.
PR	02-OCT-2000;	2000US-0236802.
PR	02-OCT-2000;	2000US-0237037.
PR	02-OCT-2000;	2000US-0237038.
PR	02-OCT-2000;	2000US-0237039.
PR	02-OCT-2000;	2000US-0237040.
PR	13-OCT-2000;	2000US-0239935.
PR	13-OCT-2000;	2000US-0239937.
PR	20-OCT-2000;	2000US-0240960.
PR	20-OCT-2000;	2000US-0241221.
PR	20-OCT-2000;	2000US-0241785.
PR	20-OCT-2000;	2000US-0241786.
PR	20-OCT-2000;	2000US-0241787.
PR	20-OCT-2000;	2000US-0241808.
PR	20-OCT-2000;	2000US-0241809.
PR	20-OCT-2000;	2000US-0241826.
PR	01-NOV-2000;	2000US-0244617.
PR	08-NOV-2000;	2000US-0246474.
PR	08-NOV-2000;	2000US-0246475.
PR	08-NOV-2000;	2000US-0246476.
PR	08-NOV-2000;	2000US-0246477.
PR	08-NOV-2000;	2000US-0246478.
PR	08-NOV-2000;	2000US-0246523.
PR	08-NOV-2000;	2000US-0246524.
PR	08-NOV-2000;	2000US-0246525.
PR	08-NOV-2000;	2000US-0246526.
PR	08-NOV-2000;	2000US-0246527.
PR	08-NOV-2000;	2000US-0246532.
PR	08-NOV-2000;	2000US-0246609.
PR	08-NOV-2000;	2000US-0246610.
PR	08-NOV-2000;	2000US-0246611.
PR	08-NOV-2000;	2000US-0246613.
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PR	17-NOV-2000;	2000US-0249217.
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PR	17-NOV-2000;	2000US-0249264.
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PR	01-DEC-2000;	2000US-0250160.
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11-DEC-2000; 2000US-0254097.
05-JAN-2001; 2001US-0259678.
XX
(HUMA-) HUMAN GENOME SCI INC.
XX
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
XX WPI; 2001-581633/65.
DR N-PSDB; ABK43654.
DR

Query Match	38.9 %;	Score 372;	DB 22;	Length 172;
Best Local Similarity	43.5 %;	Pred. No. 2.7e-32;		
Matches 77;	Conservative 36;	Mismatches 54;	Indels 10;	Gaps 3;

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Db	1	LEEYQ	A	L	T	F	L	T	R	N	E	I	L	C	I	H	D	T	L	K	L	C	P	P	G	K	Y	K	E	A	T	L	---	T	M	D	Q	V	S	S	L	P	A	L	R	V	N	P	F	R	D	R	56				
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Db	57	ICRVF	S	---	---	H	K	G	M	F	S	F	E	D	V	L	G	M	A	S	V	F	S	E	Q	A	C	P	S	L	K	I	E	Y	A	F	R	I	Y	D	N	E	N	G	F	I	D	E	D	L	Q	R	I	113			
QY	133	NCLT	G	E	G	E	D	T	R	L	S	A	E	M	K	L	I	D	N	I	L	E	S	D	I	D	R	G	T	I	N	L	S	E	F	Q	H	V	I	S	R	S	P	D	F	A	S	S	F	K	I	189					
Db	114	LRLN	S	D	---	---	M	S	E	D	L	L	M	D	T	N	H	V	L	S	E	S	D	L	D	N	D	N	M	L	S	F	S	E	F	E	H	A	M	A	K	S	P	D	E	M	N	S	F	R	167						

RESULT 5
AAM43562
ID AAM43562 standard; Protein; 184 AA.
XX
XX AAM43562;
XX AC
XX
DT 22-OCT-2001 (first entry)

XX	DE	Human polypeptide SEQ ID NO 240.
XX	KW	Human; antiarthritic; antirheumatic; antiproliferative; vasotropic;
KW	KW	cerebroprotective; nootropic; neuroprotective; antibacterial; virucide;
KW	KW	fungicide; ophthalmological; cytostatic; immunosuppressive; nootropic;
KW	KW	neuroprotective; antiallergic; hepatotropic; antidiabetic;
KW	KW	antiinflammatory; antiulcer; vulnery; anticonvulsant; antibacterial;
KW	KW	antiparasitic; cardiant; gene therapy; cancer; immune disorder;
KW	KW	cardiovascular disorder; neurological disease; infection; human.
XX	OS	Homo sapiens.
XX	PN	WO200155308-A2.
XX	PD	02-AUG-2001.
XX	PF	17-JAN-2001; 2001WO-US01309.
XX	PR	31-JAN-2000; 2000US-0179065.
PR	PR	04-FEB-2000; 2000US-0180628.
PR	PR	24-FEB-2000; 2000US-0184664.
PR	PR	02-MAR-2000; 2000US-0186350.
PR	PR	16-MAR-2000; 2000US-0189874.
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PR	PR	18-APR-2000; 2000US-0198123.
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PR	PR	07-JUL-2000; 2000US-0216647.
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PR	PR	02-OCT-2000; 2000US-0237039.
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PR	PR	20-OCT-2000; 2000US-0241787.
PR	PR	20-OCT-2000; 2000US-0241809.
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PR	PR	08-NOV-2000; 2000US-0246476.
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PR	PR	17-NOV-2000; 2000US-0249245.
PR	PR	17-NOV-2000; 2000US-0249264.
PR	PR	17-NOV-2000; 2000US-0249265.
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PR	PR	01-DEC-2000; 2000US-0250160.
PR	PR	01-DEC-2000; 2000US-0250391.
PR	PR	05-DEC-2000; 2000US-0251030.
PR	PR	05-DEC-2000; 2000US-0251988.

ABB96054
ID ABB96054 standard; Protein; 173 AA.
XX
AC ABB96054;
XX
DT 21-JUN-2002 (first entry)
XX
DE Human testicular antigen SEQ ID NO: 1438.
XX
KW Human; testicular antigen; testes; cancer; metastasis; immune disorder;
KW reproductive system disorder; urinary system disorder; gene therapy;
KW cardiovascular disorder; respiratory disorder; neurological disorder;
KW gastrointestinal disease; infection; cytostatic.
OS
XX Homo sapiens.
XX
PN WO200155317-A2.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01329.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
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PR 02-MAR-2000; 2000US-0186350.
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PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
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PR 17-NOV-2000; 2000US-0249245.
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PR 17-NOV-2000; 2000US-0249297.
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PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.

PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
PI
XX WPI; 2001-483232/52.
DR
XX Nucleic acids encoding 973 human testicular antigen polypeptides,
PT useful for preventing, diagnosing and/or treating testicular cancer
XX
XX Claim 11; SEQ ID NO 1438; 766pp; English.
PS
XX The present invention provides the protein and coding sequences of 973
CC human testicular antigens, and fragments of their genomic sequences. The
CC sequences can be used in the treatment of cardiovascular, urinary system,
CC reproductive system, immune, respiratory, neurological and
CC gastrointestinal disorders, infections, and particularly cancer,
CC especially testicular cancers. The present sequence is a protein of the
CC invention.
XX
SQ Sequence 173 AA;
Query Match 37.1%; Score 355; DB 22; Length 173;
Best Local Similarity 42.3%; Pred. No. 1.9e-30;
Matches 74; Conservative 35; Mismatches 56; Indels 10; Gaps 3;
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QY 73 ICRVFTSPAKDSLSFEDFLDLLSVFSDTATPDIKSHYAFRIPDFDDGTLNREXLSRLV 132
Db 57 ICRVFS---HKGMFSEFDVLGMASVFSEQACPSLKIEYAFRIYDFNENGFIDEEDLQRII 113
QY 133 NCLTGEGETRLSASEMKQLIDNILEESDIDRDGTINLSEFQHVLSRSPDFASSF 187
Db 114 LRLNSDD---NSEDLLMDLTNHLVLSXSDLDNDNMLSFSEFEHAMAOKSPDFMTPF 165
RESULT 8
AAU87612
ID AAU87612 standard; Protein; 173 AA.
XX
AC AAU87612;
XX
DT 05-JUN-2002 (first entry)
XX
DE Novel central nervous system protein #522.
XX Central nervous system; CNS; autoimmune disease; rheumatoid arthritis;
KW hyperproliferative disorder; neoplasm; cardiovascular disorder;
KW cardiac arrest; cerebrovascular disorder; ischaemia; angiogenesis;
KW nervous system disorder; Alzheimer's disease; AIDS; ocular disorder;
KW acquired immunodeficiency virus; dysphagia; gastrointestinal disorder;
KW adenocarcinoma; reproductive system disorder; testicular feminisation;
KW endocrine disorder; diabetes; cancer; leukaemia; neovascularisation;
KW respiratory disorder; renal disorder; kidney failure; blood disorder;
KW myocardial infarction; wound healing; cell proliferation; skin aging;
XX food additive; food preservative; gene therapy.
OS Homo sapiens.

XX
PN WO200155318-A2.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01332.
XX
PR 31-JAN-2000; 2000US-0179065.
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PR 18-APR-2000; 2000US-0198123.
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PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
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PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX

PI Rosen CA, Barash SC, Ruben SM;
XX WPI: 2001-581633/65.
DR N-PSDB; ABK43942.
DR XX

PT New isolated nucleic acid encoding a protein for diagnosing,
PT preventing, treating or ameliorating medical conditions and used as
PT food additives or preservatives
XX
PS Claim 9; SEQ ID No 1130; 837pp; English.

XX The invention describes an isolated nucleic acid molecule (I) encoding a
CC novel central nervous system protein. (I) and polypeptides (II) encoded
CC by (I), are used to treat a medical conditions and in diagnosis of a
CC pathological condition. Disorders which are diagnosed or treated include
CC autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative
CC disorders e.g. neoplasms of the breast or liver, cardiovascular disorders
CC e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischemia,
CC angiogenesis, nervous system disorders e.g. Alzheimer's disease and
CC amyotrophic lateral sclerosis, infections caused by bacteria, viruses
CC e.g. Acquired immunodeficiency virus (AIDS) and fungi, ocular disorders
CC e.g. corneal infection, gastrointestinal disorders e.g. dysphagia,
CC adenocarcinomas and irritable bowel syndrome, reproductive system
CC disorders e.g. testicular feminisation, endocrine disorders e.g. diabetes
CC and pituitary dwarfism, cancers and disorders at the cellular level e.g.
CC leukaemia, disorders involving neovascularisation e.g. malignancies,
CC respiratory disorders e.g. nonallergic rhinitis, renal disorders e.g.
CC acute kidney failure and blood related disorders e.g. myocardial
CC infarction. The polypeptides can also be used to aid wound healing and
CC epithelial cell proliferation, to prevent skin aging due to sunburn, to
CC maintain organs before transplantation, for supporting cell culture of
CC primary tissues, to regenerate tissues and in chemotaxis. The
CC polypeptides can also be used as a food additive or preservative to
CC increase or decrease storage capabilities, fat content, lipid, protein,

Query Match 37.1%; Score 355; DB 22; Length 173;
Best Local Similarity 42.3%; Pred. No. 1.9e-30;
Matches 74; Conservative 35; Mismatches 56; Indels 10; Gaps 3;

OY 13 LAEYQDITFLTKQEIILAHRRFCCLLPQEQRTVESSLRAQVFEQILSLPELKANPKER 72
Db 1 LEEYQALTEFLTRNEILCIHDTFLKCPGKYKEATL---TMDQVSSLPALRVNPFRRDR 56
OY 73 ICRVFTSPAKDSLSEFEDFLDLISVSDTATPDIKSHVAFRIEDDDGTLNREXSLRV 132
Db 57 ICRVFS--HKGMFSFEDVLGMASVSEQACPSLKIEYAFRIYDENENGFIDEDLQRII 113
OY 133 NCLTGEEDTRLASSEMQLIDNILEESDIDRDGTINLSEFOHVISRSPDFASSF 187
Db 114 LRLNSDD---MSEDLMDLTNHLVLSXSDLDNDNMLSFSEFEHAMAKSPDFMTPF 165

RESULT 9
AAM95362
ID AAM95362 standard; Protein; 173 AA.
XX
AC AAM95362;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human reproductive system related antigen SEQ ID NO: 4020.
XX
DE Human reproductive system related antigen; reproductive system disorder;
KW cancer; gene therapy.
XX
OS Homo sapiens.
XX
PN WO200155320-A2.
XX
PD 02-AUG-2001.
PF 17-JAN-2001; 2001MO-US01339.
XX

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PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
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PR 08-NOV-2000; 2000US-0246476.
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PR 17-NOV-2000; 2000US-0249209.
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PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.

(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Barash SC, Ruben SM;

WPI; 2001-465570/50.

N-PSDB; AAL01332.

is used in preventing, treating or ameliorating a medical condition

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XX PS Claim 11; SEQ ID NO 4020; 1297pp + Sequence Listing; English.
XX CC
CC The present invention provides the protein and coding sequences of a
CC number of human reproductive system related antigens. These can be used
CC in the prevention and treatment of reproductive system disorders,
CC including cancer. The present sequence is a protein of the invention.
XX
SQ Sequence 173 AA;

Query Match 37.1%; Score 355; DB 22; Length 173;
Best Local Similarity 42.3%; Pred. No. 1.9e-30;
Matches 74; Conservative 35; Mismatches 56; Indels 10; Gaps 3;

QY 13 LAEYQDLTFELTKOELLAHRRFCLELPQORTVESSLRAQVPFEQILSLPELKANPEKER 72
Db 1 LEEYQALTFELTRNEILCIHDTFLKLCPPGKYYKEATL---TMDQVSSLPALRVNPFDR 56

QY 73 ICRVFTSPAKDSLSEFEDFLDLVSFSDTATPDIKSHYAFRIEDFDDGTINREXLSRLV 132
Db 57 ICRVFS---HKGMFSFEDVLGMASVSEQACPSLKIEYAFRIYDFENGFIDEEDLQRII 113

QY 133 NCLTGECEDTRLSASEMKOLIDNILEESDIDRDGTINLSEFQHVISRSPDEASSF 187
Db 114 LRLNSDD--MSEDLMDLTNHNVSXSDLDNDNMLSFSEFEHMAKSPDEMTPF 165

RESULT 10
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ID AAM43637 standard; Protein; 173 AA.
XX
AC AAM43637;
XX
DT 22-OCT-2001 (first entry)
XX
DE Human polypeptide.SEQ ID NO 315.
XX
KW Human; antiarthritic; antirheumatic; antiproliferative; vasotropic;
KW cerebroprotective; nootropic; neuroprotective; antibacterial; virucide;
KW fungicide; ophthalmological; cytostatic; immunosuppressive; nootropic;
KW neuroprotective; antiallergic; hepatotropic; antidiabetic;
KW antiinflammatory; antitumor; antileukemic; anticonvulsant; antibacterial;
KW antiparasitic; cardiac; gene therapy; cancer; immune disorder;
KW cardiovascular disorder; neurological disease; infection; human.
XX
OS Homo sapiens.
XX
PN WO200155308-A2.
XX
PD 02-AUG-2001.
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PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 01-DEC-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 06-DEC-2000; 2000US-0256719.
PR 08-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.

(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Barash SC, Ruben SM;

WPI; 2001-465568/50.

N-PSDB; AAS31637.

Isolated nucleic acid molecule encoding a calcium-binding protein is used in preventing, treating or ameliorating a medical condition -

Claim 11; SEQ ID No 149; 542pp; English.

XX
CC The present invention relates to the isolation of novel human
CC calcium-binding proteins, and cDNA (AAS31577-AAS31654) and genomic
CC sequences encoding for these proteins. The sequences of the invention
CC are useful in the diagnosis, prevention and/or prognosis of diseases
CC associated with aberrant calcium flux. Such disorders include
CC neurological diseases (e.g. amyotrophic lateral sclerosis, ALS),
CC immune dysfunction (e.g. severe combined immunodeficiency, SCID),
CC digestive disorders (e.g. irritable bowel syndrome, IBS), neoplastic
CC disease (e.g. cancer), blood disorders (e.g. haemophilia), and/or
CC infectious disease (e.g. acquired immunodeficiency syndrome, AIDS). The
CC novel calcium-binding proteins are also useful as screening tools to
CC identify antagonists and/or agonists that may enhance or inhibit
CC activities mediated by calcium-binding proteins. The polynucleotides of
CC the invention are also useful in gene therapy. AAU19892-AAU19969
CC represent the novel human calcium-binding proteins.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

SO Sequence 173 AA;

Query Match 37.1%; Score 355; DB 22; Length 173;
Best Local Similarity 42.3%; Pred. No. 1.9e-30;
Matches 74; Conservative 35; Mismatches 56; Indels 10; Gaps 3;

AAX40438 to AAX40715 represent 5' expressed sequence tags (ESTs) for human secreted proteins expressed in prostate, and encode the proteins given in AAY11716 to AAY11993 respectively. The proteins given represent the signal peptide and an N-terminal fragment of a secreted protein. The nucleic acid sequences can be used for producing secreted human gene products. They can also be used to develop products for diagnosis and therapy. The proteins obtained may have cytokine activity, cell proliferation and differentiation activity, haematopoiesis regulating activity, tissue growth regulating activity, reproductive hormone regulating activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, receptor/ligand activity, anti-inflammatory activity, tumour inhibition activity or other activities. The products can be used in forensic, gene therapy and chromosome mapping procedures. The sequences can also be used for obtaining corresponding promoter sequences. The nucleic acids encoding the signal peptides can be used for directing extracellular secretion of a polypeptide or the insertion of a polypeptide into a membrane, or importing a polypeptide into a cell.

Sequence	120 AA;
SQ	

Query Match 23.0%; Score 220; DB 20; Length 120;
Best Local Similarity 66.2%; Pred. No. 5.7e-16;
Matches 45; Conservative 4; Mismatches 19; Indels 0; Gaps 0;

QY	1	MGGSGSRLSKELLA	EYQDLTFLTKQEILLAHRRFC	ELLPQEQR	TVESSLR	AQVPFEQILS	60
	.						:
	.						: :
Dd	1	MGGSGSRLSKELLA	EYQDLTFLTKQEILLAHRRFC	ELLPQEQR	XXXSRHFGHKC	PSSRFS	60

Qy 61 LPPEKANP 68

Db 61 FQSSRPTP 68

Search completed: January 17, 2003, 12:43:08
Job time : 36 secs

Sequence 2, Application US/09878454A
GENERAL INFORMATION:
APPLICANT: Monteiro, et al.
TITLE OF INVENTION: Method of Controlling the Binding of Calmyrin to Presentlin
FILE REFERENCE: 4115-161
CURRENT APPLICATION NUMBER: US/09/878,454A
CURRENT FILING DATE: 2001-06-11
PRIOR APPLICATION NUMBER: 60/210,939
PRIOR FILING DATE: 2000-06-11
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 191
TYPE: PRT
ORGANISM: Homo sapiens
MUT127
MGSGSRLSKELLAAYQDLTFLTKQEIILAHRRCELLPOEORTVESSLRAQVPEQILSLPELKANPER
ERICRVSTSPAKDLSFEDFLDLVSFSDTATPDIKSHYAFRIFFEDDGTLNREXLSRLVNCILTGEGE
DTRLASSEMQLIDNILEESDIDRDGTINSEFQHVISRSPDFASSRTIVLI

psn127
5D

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 17, 2003, 12:47:34 ; Search time 15 Seconds
(without alignments)
374.652 Million cell updates/sec

Title: MUT127
Perfect score: 957
Sequence: 1 MGGSGSRLSKELLAAYQDLT.....EFQHVISRSPDFASSFKIVL 191

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*

1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/Backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	953	99.6	191	4	US-08-720-625-2 Sequence 2, Appl
2	928	97.0	191	3	US-08-764-563-1 Sequence 1, Appl
3	215.5	22.5	177	3	US-08-764-563-3 Sequence 1, Appl
4	203.5	21.3	174	1	US-08-328-322-17 Sequence 3, Appl
5	192.5	20.1	157	1	US-08-328-322-15 Sequence 17, Appl
6	185.5	19.4	169	4	US-08-720-625-4 Sequence 15, Appl
7	185.5	19.4	170	3	US-08-764-563-5 Sequence 4, Appl
8	175	18.3	186	3	US-08-655-352-8 Sequence 5, Appl
9	175	18.3	186	4	US-09-258-016-8 Sequence 8, Appl
10	175	18.3	186	4	US-09-257-825B-8 Sequence 8, Appl
11	171.5	17.9	179	3	US-08-764-563-4 Sequence 4, Appl
12	152.5	15.9	196	3	US-09-048-889-1 Sequence 1, Appl
13	149	15.6	193	3	US-08-655-352-3 Sequence 3, Appl
14	149	15.6	193	4	US-09-258-016-3 Sequence 3, Appl
15	149	15.6	193	4	US-09-257-825B-3 Sequence 3, Appl
16	142	14.8	220	4	US-09-399-913-26 Sequence 26, Appl
17	142	14.7	220	4	US-09-298-731-26 Sequence 26, Appl
18	141	14.7	191	3	US-08-655-352-7 Sequence 7, Appl
19	141	14.7	191	4	US-09-258-016-7 Sequence 7, Appl
20	141	14.7	191	4	US-09-257-825B-7 Sequence 7, Appl
21	138	14.4	193	3	US-08-655-352-2 Sequence 2, Appl
22	138	14.4	193	4	US-09-257-825B-2 Sequence 2, Appl
23	137	14.3	216	4	US-09-399-913-6 Sequence 6, Appl
24	137	14.3	216	4	US-09-399-913-6 Sequence 6, Appl
25	137	14.3	216	4	US-09-399-913-6 Sequence 6, Appl
26	137	14.3	216	4	US-09-399-913-6 Sequence 6, Appl
27	137	14.3	220	4	US-09-298-731-24 Sequence 24, Appl

28	137	14.3	227	4	US-09-399-913-8 Sequence 8, Appl
29	137	14.3	227	4	US-09-399-913-10 Sequence 10, Appl
30	137	14.3	227	4	US-09-298-731-8 Sequence 8, Appl
31	137	14.3	227	4	US-09-298-731-10 Sequence 10, Appl
32	137	14.3	245	4	US-09-399-913-4 Sequence 4, Appl
33	137	14.3	245	4	US-09-298-731-4 Sequence 4, Appl
34	137	14.3	252	4	US-09-399-913-20 Sequence 20, Appl
35	137	14.3	252	4	US-09-298-731-20 Sequence 20, Appl
36	137	14.3	270	4	US-09-399-913-14 Sequence 14, Appl
37	137	14.3	270	4	US-09-298-731-14 Sequence 14, Appl
38	136	14.2	216	4	US-09-399-913-2 Sequence 2, Appl
39	136	14.2	216	4	US-09-399-913-2 Sequence 2, Appl
40	134	14.0	270	4	US-09-298-731-18 Sequence 18, Appl
41	134	14.0	270	4	US-09-298-731-18 Sequence 18, Appl
42	133	13.9	193	3	US-08-655-352-4 Sequence 4, Appl
43	133	13.9	193	4	US-09-257-825B-4 Sequence 4, Appl
44	133	13.9	193	4	US-09-257-825B-4 Sequence 4, Appl
45	132	13.8	191	3	US-08-655-352-5 Sequence 5, Appl

ALIGNMENTS

RESULT 1
US-08-720-625-2
Sequence 2, Application US/08720625
Patent No. 6242587

GENERAL INFORMATION:
APPLICANT: Nalk, Ulhas P.
TITLE OF INVENTION: CALCIUM-INTEGRIN BINDING PROTEIN
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESS: Bell, Seltzer, Park & Gibson
STREET: P.O. Drawer 34009
CITY: Charlotte
STATE: No. 6242587th Carolina
COUNTRY: USA
ZIP: 28234

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/720,625
FILING DATE:
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5470-138
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-881-3175
TELEFAX: 919-420-2200

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 191 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-720-625-2

Query Match
Best Local Similarity 99.6%; Score 953; DB 4; Length 191;
Matches 189; Conservative 2; Mismatches 0; Indels 0; Gaps 0

QY 1 MGGSGSRLSKELLAAYQDLTFLTKQELLHAHRCCELLPQORTVSSSLRAQVPFEQITLS 60
Db 1 MGGSGSRLSKELLAAYQDLTFLTKQELLHAHRCCELLPQORTVSSSLRAQVPFEQITLS 60
QY 61 LPELKANPEKERICRVFSTSPAKDSLSFEDFLDLVSFSDTATPDIKSHYAFRFDDEDF 60

Db 61 LPPEKAPFKERICRVFSTSPAKDSLSFEDFLDLLSVFSDTATPDIKSHYAFRIFDDEDD 120

QY 121 GTLNREXLSRLVNLCTGEGEDTRLSASEMKQLIDNILEESDIDRDGTINLSEFQHVISR 180

Db 121 GTLNREXLSRLVNLCTGEGEDTRLSASEMKQLIDNILEESDIDRDGTINLSEFQHVISR 180

QY 181 PDFASSFKIVL 191

Db 181 PDFASSFKIVL 191

RESULT 2

US-08-764-563-1

; Sequence 1, Application US/08764563

; Patent No. 6093565

; GENERAL INFORMATION:

; APPLICANT: Hillman, Jennifer L.

; APPLICANT: Goli, Surya K.

; TITLE OF INVENTION: A NOVEL PROTEIN PHOSPHATASE

; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:

; STREET: 3174 Porter Drive

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08764,563

; FILING DATE: Herewith

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Billings, Lucy J.

; REGISTRATION NUMBER: 36,749

; REFERENCE/DOCKET NUMBER: PF-0178 US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-855-0555

; TELEFAX: 415-845-4166

; TELEX:

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 191 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; IMMEDIATE SOURCE:

; LIBRARY: Consensus

; CLONE: Consensus

US-08-764-563-1

Query Match 97.0%; Score 928; DB 3; Length 191;

Best Local Similarity 98.4%; Pred. No. 3.3e-93;

Matches 188; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MGGSGSRLSKELLAQYQDLTFLTKQEILLAHRRFCELLPQEQRTVLESSLRAQVPEQILS 60

Db 1 MGGSGSRLSKELLAQYQDLTFLTKQEILLAHRRFCELLPQEQRTVLESSLRAQVPEQILS 60

QY 61 LPPEKAPFKERICRVFSTSPAKDSLSFEDFLDLLSVFSDTATPDIKSHYAFRIFDDEDD 120

Db 61 LPPEKAPFKERICRVFSTSPAKDSLSFEDFLDLLSVFSDTATPDIKSHYAFRIFDDEDD 120

QY 121 GTLNREXLSRLVNLCTGEGEDTRLSASEMKQLIDNILEESDIDRDGTINLSEFQHVISR 180

Db 121 GTLNREXLSRLVNLCTGEGEDTRLSASEMKQLIDNILEESDIDRDGTINLSEFQHVISR 180

QY 181 PDFASSFKIVL 191

Db 181 PDFASSFKIVL 191

RESULT 3

US-08-764-563-3

; Sequence 3, Application US/08764563

; Patent No. 6093565

; GENERAL INFORMATION:

; APPLICANT: Hillman, Jennifer L.

; APPLICANT: Goli, Surya K.

; TITLE OF INVENTION: A NOVEL PROTEIN PHOSPHATASE

; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Incyte Pharmaceuticals, Inc.

; STREET: 3174 Porter Drive

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08764,563

; FILING DATE: Herewith

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Billings, Lucy J.

; REGISTRATION NUMBER: 36,749

; REFERENCE/DOCKET NUMBER: PF-0178 US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-855-0555

; TELEFAX: 415-845-4166

; TELEX:

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 177 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; IMMEDIATE SOURCE:

; LIBRARY: GenBank

; CLONE: 458230

US-08-764-563-3

Query Match 22.5%; Score 215.5; DB 3; Length 177;

Best Local Similarity 29.2%; Pred. No. 8.9e-16;

Matches 52; Conservative 40; Mismatches 73; Indels 13; Gaps 3;

QY 1 MGGSGSRLSKELLAQYQDLTFLTKQEILLAHRRFCELLPQEQRTVLESSLRAQVPEQILS 60

Db 1 MGTNTSSLRPEEVEEMQKGTNFTQKEIKKLYKRFKKLDKDGNGTISK-----DEFLM 52

QY 61 LPPEKAPFKERICRVFSTSPAKDSLSFEDFLDLLSVFSDTATPDIKSHYAFRIFDDEDD 120

Db 53 IPELAVNPLVLRVISIFDEN-GDGSVNFKEFIAALSVAQDKQKLEFAFKVIDDGD 111

QY 121 GTLNREXLSRLVNLCTGEGEDTRLSASEMKQLIDNILEESDIDRDGTINLSEFQHVISR 178

Db 112 GYISNGELFTVLKMMVG-----NNLSDVQLQIQIVDKTLEADEDDGDKISFEFAKTLS 165

RESULT 4

US-08-328-322-17

; Sequence 17, Application US/08328322

Patent No. 5723436
GENERAL INFORMATION:
APPLICANT: Huang, Laiqiang
APPLICANT: Cyert, Martha S.
TITLE OF INVENTION: Calcineurin Interacting Protein Compositions
TITLE OF INVENTION: and Methods
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/328,322
FILING DATE: 24-OCT-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: P38,615
REFERENCE/DOCKET NUMBER: 8600-0151.10
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-328-322-17

Query Match 21.3%; Score 203.5; DB 1; Length 174;
Best Local Similarity 27.1%; Pred. No. 1.8e-14;
Matches 48; Conservative 44; Mismatches 68; Indels 17; Gaps 4;

QY 1 MGSGSRLSKELLAAYQDLFLTKQELLHAHRRFCCLLPQEQRTVESSLRAQVPFEQILS 60
DB 1 MGAAPSKIYDGLLED---TNDRDEIERLRKRKRMKLDRSSGSIDKN-----EFMS 48

QY 61 LPELKNPFKERICRVSTSPAKDLSFEDFLDLLSVESDTPATPDIKSHYAFRIEDDD 120
DB 49 IPGVSSNPLAGRIMEVFADNSGD-VDFQEFITGLSIFSGRSKDEKLRFAPKTYDIDKD 107

QY 121 GTLNREXLSRLVNCLTGEGEDTRLASASEMKQLIDNILESDIDRDGTINLSEFQHYI 177
DB 108 GFISNGELFIVLKIMVG---SNLDEQLOQIVDRITVENSDGDGRLSFEEFKNAI 160

RESULT 5
US-08-328-322-15
Sequence 15, Application US/08328322
Patent No. 5723436
GENERAL INFORMATION:
APPLICANT: Huang, Laiqiang
APPLICANT: Cyert, Martha S.
TITLE OF INVENTION: Calcineurin Interacting Protein Compositions
TITLE OF INVENTION: and Methods
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/328,322
FILING DATE: 24-OCT-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: P38,615
REFERENCE/DOCKET NUMBER: 8600-0151.10
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 157 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-328-322-15

Query Match 20.1%; Score 192.5; DB 1; Length 157;
Best Local Similarity 27.3%; Pred. No. 2.4e-13;
Matches 42; Conservative 40; Mismatches 59; Indels 13; Gaps 3;

QY 24 KOELLHAHRRFCCLLPQEQRTVESSLRAQVPFEQILSPELKNPFKERICRVSTSPAK 83
DB 3 RDEIERLRKRKRMKLDRSSGSIDKN-----EFMSIPGVSSNPLAGRIMEVFADNSG 54

QY 84 DLSFEDFLDLLSVESDTPATPDIKSHYAFRIEDDDGTNLNREXLSRLVNCLTGEGEDTR 143
DB 55 D-VDFQEFITGLSIFSGRSKDEKLRFAPKTYDIDKDFISNGELFIVLKIMVG---SN 109

QY 144 LSASEMKQLIDNILESDIDRDGTINLSEFQHYI 177
DB 110 LDDEQLOQIVDRITVENSDGDGRLSFEEFKNAI 143

RESULT 6
US-08-720-625-4
Sequence 4, Application US/08720625
Patent No. 6242587
GENERAL INFORMATION:
APPLICANT: Naik, Uhas P.
APPLICANT: Parise, Leslie V.
TITLE OF INVENTION: CALCIUM-INTEGRIN BINDING PROTEIN
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bell, Seltzer, Park & Gibson
STREET: P.O. Drawer 34009
CITY: Charlotte
STATE: No. 6242587th Carolina
COUNTRY: USA
ZIP: 28234
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/720,625
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5470-138
TELEPHONE: 919-420-2200
TELEFAX: 919-881-3175
INFORMATION FOR SEQ ID NO: 4:

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Best Local Similarity   31.1%; Pred. No. 1.5e-12;
Matches    38; Conservative   32; Mismatches   47; Indels      5; Gaps       2;

QY  56 EQILSPELKANPFKERICRVFSTSPAKDSLSFEFLDLLSVFSDTATPDIKSHYAFRIF 115
   : : ||||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db  41 EEFMSLPQLQNPLVQRVIDIFTD-GNGEVDKFKEFIGVSQFSVKGDKEQKLRFARIY 99

QY  116 DFDDDGTLNREXLSRLVNCLTGEGETRSLASEMKQLIDNILEESDIDRDGTINLSEFOH 175
   | | ||| :: | : | : | : | : | : | : | : | : | : | : | : | : |
Db  100 DMDKDGYISNGELFQVLKMVG-----NNLKDTQLQQIVDKTIINADKGDGRISFEFCFA 155

QY  176 VI 177
   :-
Db  156 VV 157

RESULT 8
US-08-655-352-8
; Sequence 8, Application US/08655352
; Patent No. 6077991
; GENERAL INFORMATION:
; APPLICANT: Bachetira W. Poovaiiah, Zhihua Liu,
; APPLICANT: Shameekumar Patil, Daisuke Takezawa
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: PRODUCTION OF MALE-STERILE PLANTS
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Klarquist Sparkman Campbell Leigh &
; ADDRESSEE: Whinston, LLP
; STREET: One World Trade Center
; STREET: 121 S.W. Salmon Street
; STREET: Suite 1600
; CITY: Portland
; STATE: Oregon
; COUNTRY: United States of America
; ZIP: 97204
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Disk, 3-1/2 inch
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/655,352
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/323,449
; FILING DATE: October 14, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Dow, Alan. E.
; REGISTRATION NUMBER: 35,123
; REFERENCE/DOCKET NUMBER: 4630-45000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (503) 226-7391
; TELEFAX: (503) 228-9446
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 186 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; DESCRIPTION: Region of Drosophila frequenin
; DESCRIPTION: (Gen2:Drofreg) with homology to lily
; DESCRIPTION: CCAMK
;
US-08-655-352-8
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OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/764,563
FILING DATE: Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0178 US
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 179 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 109612
US-08-764-563-4

Query Match : 17.9%; Score 171.5; DB 3; Length 179;
Best Local Similarity 27.8%; Pred. No. 5.5e-11;
Matches 42; Conservative 30; Mismatches 66; Indels 13; Gaps 3;
QY 35 CELLPQE-----RTVESSLRAQVPFEQILSLPELKANPFKERICRVFSTSPAKDSL 86
Db 12 CNHFDQEEIRRLGKSRKLDLXSGSLSEIEFMRLPELQONPLVGRVIDIFDFTD-GNGEV 70
QY 87 SFEDFLDLLSVFSPATPDIKSHYAFRIFDDGTLNREXLSRLVNLCTGEGEDTRLSA 146
Db 71 DFHEFVGTQSFVKGDEEQKLRFAFRFYDNDGDFISNGELFQVLKMMVG----NNLKD 126
QY 147 SEMQLIDNILEESDIDRDGTINLSEFQHVI 177
Db 127 WQLQQLVDKSLVLDKDGGRISFEFSDV 157

RESULT 12
US-09-048-889-1
Sequence 1, Application US/09048889
Patent No. 6117989
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer L.
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
APPLICANT: Lal, Preeti
APPLICANT: Patterson, Chandra
TITLE OF INVENTION: HUMAN CALCIUM-BINDING PROTEINS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/048,889
FILING DATE: Herewith

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Cerrone, Michael C
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0493 US
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 196 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: COLNOT09
CLONE: 1846517
US-09-048-889-1

Query Match : 15.9%; Score 152.5; DB 3; Length 196;
Best Local Similarity 23.3%; Pred. No. 7.3e-09;
Matches 44; Conservative 39; Mismatches 73; Indels 33; Gaps 6;
QY 5 GSRLSKELLAQYQDL---TFLTKQEILLAHRRFCELLPQEQRTVESSLRAQVPFEQILS 60
Db 2 GSRTSHAAVDPDGSIRRETGFSQASLLRLHRRF-----RALDRNKKGYSRMDLQQ 53
QY 61 LPELKANPFKERICRVFSTSPAKDSLSFEDFLDLLSVF-----SDTATPDIKS----- 108
Db 54 IGALAVNPLGDRHIESFFPG-GSQRVDFPGFVRVLAHFRPVEDEDTETQDPKKPEPLNSR 112
QY 109 ----HYAFRIFDDGTLNREXLSRLVNLCTGEGEDTRLSASEMKQLIDNILEESDIDR 164
Db 113 RNKLHYAFQLYDLDRDGKISRHEMLQVLRMLVG----VQVTEQLENIADRTVQEADEG 168
QY 165 DGTINLSEF 173
Db 169 DGAVSFEV 177

RESULT 13
US-08-655-352-3
Sequence 3, Application US/08655352
Patent No. 6077991
GENERAL INFORMATION:
APPLICANT: Bachettira W. Poovalah, Zhihua Liu,
APPLICANT: Shameekumar Patil, Daisuke Takezawa
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
PRODUCTION OF MALE-STERILE PLANTS
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klarquist Sparkman Campbell Leigh &
ADDRESSEE: Winston, LLP
STREET: One World Trade Center
STREET: 121 S.W. Salmon Street
STREET: Suite 1600
CITY: Portland
STATE: Oregon
COUNTRY: United States of America
ZIP: 97204
COMPUTER READABLE FORM:
MEDIUM TYPE: Disk, 3-1/2 inch
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/655,352
FILING DATE:
CLASSIFICATION: 800

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/323,449
;; FILING DATE: October 14, 1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Dow, Alan. E.
;; REGISTRATION NUMBER: 35,123
;; REFERENCE/DOCKET NUMBER: 4630-45000
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (503) 226-7391
;; TELEFAX: (503) 228-9446
;; INFORMATION FOR SEQ ID NO: 3:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 193 amino acids
;; TYPE: amino acid
;; TOPOLOGY: 1linear
;; MOLECULE TYPE: protein
;; DESCRIPTION: Region of rat neural visinin-like protein
;; DESCRIPTION: (Gen2:Ratnvp3) with homology to 11ly
;; DESCRIPTION: CCAMK
US-08-655-352-3

Query Match 15.6%; Score 149; DB 3; Length 193;
Best Local Similarity 24.5%; Pred. No. 1.7e-08;
Matches 51; Conservative 42; Mismatches 79; Indels 36; Gaps 7;

QY 1 MGGSGSRLSKELLAERYODLFTLKQEILLAHRRFCCELLPOEQRTVESSLRAQVPEQILS 60
Db 1 MGKONSKLRPEVLQDLREHTEFTDHELQEWYKGLKDCPTGHLTVDE-----FKKIYA 53

QY 61 --LPELKANPFKERICRVFSTSPAKDSLSFEDFLDLLSVFSDDTATPDIKSHYAFRIFFD 118
Db 54 NEFPYGDASKFAEHVFRFTDIN-SDGTIDFREFFIALSVTS-RGKLEQIKWAFSMYDLD 111

QY 119 DDGTLNREXLSRLVNCLTGEGEDTRLASASEM-----QLIDNILEESDIDRDGTIN 169
Db 112 GNGYISRSEMLEIVQAI-----YKVVSSVMKMPEDESTPEKRTDKIFROMDINNKGKLS 165

QY 170 LSEF-----QHVISRSPDFASSF 187
Db 166 LEEFIKAKSDPSIVRLQCDPSSASQF 193

RESULT 14
US-09-258-016-3
; Sequence 3, Application US/09258016
; Patent No. 6362395
; GENERAL INFORMATION:
; APPLICANT: Bachettlira W. Poovaiyah, Zhilhua Liu,
; APPLICANT: Shameekumar Patil, Daisuke Takezawa
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: PRODUCTION OF MALE-STERILE PLANTS
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kiarquist, Sparkman Campbell Leigh &
; ADDRESSEE: Winston, LLP
; STREET: One World Trade Center
; STREET: 121 S.W. Salmon Street
; STREET: Suite 1600
; CITY: Portland
; STATE: Oregon
; COUNTRY: United States of America
; ZIP: 97204
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Disk, 3-1/2 inch.
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/258, 016
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Stephens Jr., Donald L.

;; REGISTRATION NUMBER: 34,022
;; REFERENCE/DOCKET NUMBER: 4630-51994
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (503) 226-7391
;; TELEFAX: (503) 228-9446
;; INFORMATION FOR SEQ ID NO: 3:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 193 amino acids
;; TYPE: amino acid
;; TOPOLOGY: 1linear
;; MOLECULE TYPE: protein
;; DESCRIPTION: Region of rat neural visinin-like protein
;; DESCRIPTION: (Gen2:Ratnvp3) with homology to 11ly
;; DESCRIPTION: CCAMK
US-09-258-016-3

Query Match 15.6%; Score 149; DB 4; Length 193;
Best Local Similarity 24.5%; Pred. No. 1.7e-08;
Matches 51; Conservative 42; Mismatches 79; Indels 36; Gaps 7;

QY 1 MGGSGSRLSKELLAERYODLFTLKQEILLAHRRFCCELLPOEQRTVESSLRAQVPEQILS 60
Db 1 MGKONSKLRPEVLQDLREHTEFTDHELQEWYKGLKDCPTGHLTVDE-----FKKIYA 53

QY 61 --LPELKANPFKERICRVFSTSPAKDSLSFEDFLDLLSVFSDDTATPDIKSHYAFRIFFD 118
Db 54 NEFPYGDASKFAEHVFRFTDIN-SDGTIDFREFFIALSVTS-RGKLEQIKWAFSMYDLD 111

QY 119 DDGTLNREXLSRLVNCLTGEGEDTRLASASEM-----QLIDNILEESDIDRDGTIN 169
Db 112 GNGYISRSEMLEIVQAI-----YKVVSSVMKMPEDESTPEKRTDKIFROMDINNKGKLS 165

QY 170 LSEF-----QHVISRSPDFASSF 187
Db 166 LEEFIKAKSDPSIVRLQCDPSSASQF 193

RESULT 15
US-09-257-825B-3
; Sequence 3, Application US/09257825B
; Patent No. 6403352
; GENERAL INFORMATION:
; APPLICANT: Poovaiyah, Bachettlira W.
; APPLICANT: Patil, Shameekumar
; APPLICANT: Takezawa, Daisuke
; TITLE OF INVENTION: Compositions and Methods for Production of Male-Sterile Plant
; FILE REFERENCE: 4630-51993
; CURRENT APPLICATION NUMBER: US/09/257, 825B
; CURRENT FILING DATE: 1999-02-25
; PRIOR APPLICATION NUMBER: US 08/655, 352
; PRIOR FILING DATE: 1996-05-23
; PRIOR APPLICATION NUMBER: US 60/014, 743
; PRIOR FILING DATE: 1996-03-28
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Rat
US-09-257-825B-3

Query Match 15.6%; Score 149; DB 4; Length 193;
Best Local Similarity 24.5%; Pred. No. 1.7e-08;
Matches 51; Conservative 42; Mismatches 79; Indels 36; Gaps 7;

QY 1 MGGSGSRLSKELLAERYODLFTLKQEILLAHRRFCCELLPOEQRTVESSLRAQVPEQILS 60
Db 1 MGKONSKLRPEVLQDLREHTEFTDHELQEWYKGLKDCPTGHLTVDE-----FKKIYA 53

QY 61 --LPELKANPFKERICRVFSTSPAKDSLSFEDFLDLLSVFSDDTATPDIKSHYAFRIFFD 118
Db 54 NEFPYGDASKFAEHVFRFTDIN-SDGTIDFREFFIALSVTS-RGKLEQIKWAFSMYDLD 111

QY 119 DDGTLNREXLRLVNC LTGEGEDTRL SASEMK-----QLIDNILEESDIDRDGTIN 169
Db 112 GNGYISRSEMLEIVQAI-----YKMVSSVMKMPEDSTPEKRTDKIFRQMDINNDGKLS 165
QY 170 LSEF-----QHVISRSPDFASSE 187
Db 166 LEEFIKGAKSDPSIVRLQLQCDPSSASQF 193

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mutation at psu127

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 17, 2003, 12:42:28 ; Search time 11 Seconds

(without alignments)
345.163 Million cell updates/sec

Title: MUT127
Perfect score: 957
Sequence: 1 MGSGSRLSKELLAERYDILT.....EFQHVISRSPDFASSFKIVL 191

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 120991 seqs, 19878514 residues

Total number of hits satisfying chosen parameters: 120991

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*

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2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
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9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
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11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
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13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	955	99.8	191	10 US-09-878-454A-2	Sequence 2, Appl1
2	943	98.5	191	12 US-10-109-885-2	Sequence 2, Appl1
3	338	35.3	187	10 US-09-802-116-2	Sequence 2, Appl1
4	183.5	19.2	170	12 US-10-109-885-3	Sequence 3, Appl1
5	176.5	18.4	195	10 US-09-999-602-3	Sequence 3, Appl1
6	171.5	17.9	195	10 US-09-999-602-4	Sequence 4, Appl1
7	140	14.6	220	10 US-09-350-874-26	Sequence 26, Appl1
8	135	14.1	216	10 US-09-350-874-6	Sequence 6, Appl1
9	135	14.1	220	10 US-09-350-874-24	Sequence 24, Appl1
10	135	14.1	227	10 US-09-350-874-8	Sequence 8, Appl1
11	135	14.1	227	10 US-09-350-874-10	Sequence 10, Appl1
12	135	14.1	245	10 US-09-350-874-4	Sequence 4, Appl1
13	135	14.1	252	10 US-09-350-874-20	Sequence 20, Appl1
14	135	14.1	270	10 US-09-350-874-14	Sequence 14, Appl1
15	134	14.0	216	9 US-09-965-528-15	Sequence 15, Appl1
16	134	14.0	216	10 US-09-350-874-2	Sequence 2, Appl1
17	133.5	13.9	214	10 US-09-999-602-1	Sequence 1, Appl1
18	132	13.8	270	10 US-09-350-874-18	Sequence 18, Appl1
19	130	13.6	225	10 US-09-350-874-30	Sequence 30, Appl1

20	130	13.6	252	10 US-09-350-874-22	Sequence 22, Appl1
21	130	13.6	252	10 US-09-350-874-28	Sequence 28, Appl1
22	130	13.6	252	10 US-09-350-874-42	Sequence 42, Appl1
23	130	13.6	257	10 US-09-350-874-16	Sequence 16, Appl1
24	120	12.5	229	10 US-09-350-874-70	Sequence 70, Appl1
25	120	12.5	233	10 US-09-350-874-49	Sequence 49, Appl1
26	120	12.5	250	10 US-09-350-874-72	Sequence 72, Appl1
27	110.5	11.5	172	12 US-10-109-885-4	Sequence 4, Appl1
28	110.5	11.5	1210	9 US-10-025-380-692	Sequence 692, App
29	110.5	11.5	1210	10 US-09-922-217-692	Sequence 692, App
30	110.5	11.5	1210	10 US-09-833-263-692	Sequence 692, App
31	110.5	11.5	1548	9 US-10-025-380-1095	Sequence 1095, Ap
32	110.5	11.5	1548	10 US-09-922-217-1095	Sequence 1095, Ap
33	109	11.4	256	10 US-09-350-874-32	Sequence 32, Appl1
34	108.5	11.3	142	10 US-09-910-071-4	Sequence 4, Appl1
35	108	11.3	642	9 US-09-554-000-6	Sequence 6, Appl1
36	108	11.3	656	9 US-09-554-000-8	Sequence 8, Appl1
37	107	11.2	203	10 US-09-350-874-12	Sequence 12, Appl1
38	107	11.2	642	9 US-09-554-000-2	Sequence 2, Appl1
39	107	11.2	652	9 US-09-554-000-4	Sequence 4, Appl1
40	106	11.1	256	10 US-09-350-874-36	Sequence 36, Appl1
41	105.5	11.0	201	10 US-09-925-297-714	Sequence 714, App
42	104.5	10.9	159	10 US-09-910-071-5	Sequence 5, Appl1
43	99.5	10.4	139	10 US-09-864-761-34808	Sequence 34808, A
44	93.5	9.8	171	9 US-09-981-353-161	Sequence 161, App
45	92.5	9.7	90	10 US-09-826-589-3	Sequence 3, Appl1

ALIGNMENTS

RESULT 1
US-09-878-454A-2
Sequence 2, Application US/09878454A
Patent No. US20020064828A1
GENERAL INFORMATION:
APPLICANT: Monteliro, et al.
TITLE OF INVENTION: Method of Controlling the Binding of Calmyrin to Present11n
FILE REFERENCE: 4115-161
CURRENT APPLICATION NUMBER: US/09/878,454A
CURRENT FILING DATE: 2001-06-11
PRIOR APPLICATION NUMBER: 60/210,939
PRIOR FILING DATE: 2000-06-11
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 191
TYPE: PRT
ORGANISM: Homo sapiens
US-09-878-454A-2

Query Match	99.8%	Score 955;	DB 10;	Length 191;
Best Local Similarity	99.5%	Pred. No. 1.6e-89;		
Matches 190;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
QY	1	MGSGSRLSKELLAERYDITFLTKOEILAHRRCELLPQEQRTVESSLRAQVFEQILS 60		
DB	1	MGSGSRLSKELLAERYDITFLTKOEILAHRRCELLPQEQRTVESSLRAQVFEQILS 60		
QY	61	LPFLKANPFEKRICRYFSTSPAKDSLSEFDFLDLSVFSSTATPDIKSHYAFRIFFDDDD 120		
DB	61	LPFLKANPFEKRICRYFSTSPAKDSLSEFDFLDLSVFSSTATPDIKSHYAFRIFFDDDD 120		
QY	121	GTLNREXLSRLVNCITGEGEDTRLSSASEMKQILDNILESDDIDRDGTINSEFQHVISR 180		
DB	121	GTLNREXLSRLVNCITGEGEDTRLSSASEMKQILDNILESDDIDRDGTINSEFQHVISR 180		
QY	181	PDFASSFKIVL 191		
DB	181	PDFASSFKIVL 191		
RESULT 2				

US-10-109-885-2
; Sequence 2, Application US/10109885
; Patent No. US20020119129A1
; GENERAL INFORMATION:
; APPLICANT: REVEL, Michel
; APPLICANT: CHEBATH, Judith
; APPLICANT: ABRAMOVITCH, Carolina
; TITLE OF INVENTION: NOVEL IFN RECEPTOR I BINDING PROTEIN, DNA ENCODING THEM, AND METH
; TITLE OF INVENTION: MODULATING CELLULAR RESPONSE TO INTERFERON
; FILE REFERENCE: REVEL-14A
; CURRENT APPLICATION NUMBER: US/10/109,885
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: US/09/341,640
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: PCT/US98/00671
; PRIOR FILING DATE: 1998-01-15
; PRIOR APPLICATION NUMBER: US 60/035,636
; PRIOR FILING DATE: 1997-01-15
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 191
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-109-885-2

Query Match 98.5%; Score 943; DB 12; Length 191;
Best Local Similarity 98.4%; Pred. No. 2.6e-88;
Matches 188; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 MGGSGRSLKELLAQYQDLTFLTKQEIILAHRRFCELLPQEQRTVSSSLRAQVPFEQILS 60
Db 1 MGGSGRSLKELLAQYQDLTFLTKQEIILAHRRFCELLPQEQRSVSSSLRAQVPFEQILS 60
QY 61 LPELKANPFKERICRVFSTSPAKDSLSFEDFLDLSVFSDTATPDIKSHYAFRIEFD 120
Db 61 LPELKANPFKERICRVFSTSPAKDSLSFEDFLDLSVFSDTATPDIKSHYAFRIEFD 120
QY 121 GTLNREXLSRLVNCLTGEGEDTRLSASEMKQLIDNILEESDIDRDGTINLSEFQHV 180
Db 121 GTLNREXLSRLVNCLTGEGEDTRLSASEMKQLIDNILEESDIDRDGTINLSEFQHV 180
QY 181 PDFASSFKIVL 191
Db 181 PDFASSFKIVL 191

RESULT 3
US-09-802-116-2
; Sequence 2, Application US/09802116
; Patent No. US20020082406A1
; GENERAL INFORMATION:
; APPLICANT: Mathur, Brian
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. US20020082406A1 Human Kinase Interacting Protein and Polynu
; TITLE OF INVENTION: the Same
; FILE REFERENCE: LEX-0146-USA
; CURRENT APPLICATION NUMBER: US/09/802,116
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 60/187,719
; PRIOR FILING DATE: 2000-03-08
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 187
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-802-116-2

Query Match 35.3%; Score 338; DB 10; Length 187;
Best Local Similarity 39.9%; Pred. No. 4.5e-27;
Matches 77; Conservative 42; Mismatches 62; Indels 12; Gaps 5;

QY 1 MGGSGRSLKELLAQYQDLTFLTKQEIILAHRRFCELLPQEQRTVSSSLRAQVPFE 56
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QY 57 QILSLPELKANPFKERICRVFSTSPAKDSLSFEDFLDLSVFSDTATPDIKSHYAFRIE 116
Db 58 LIGSMPKDNPFQRORIAQVFS-EDGDGHMTLDNFDLMSVMSEMAPRDLKAYYAFKIYD 116
QY 117 FDDDGTLNREXLSRLVNCLTGEGEDTRLSASEMKQLIDNILEESDIDRDGTINLSEFQHV 176
Db 117 FNNDYYICAWDLEQTVTKLT-RGE---LSAEVSLVCEKVLDEADGDHGDGRSLSEDFQNM 172
QY 177 ISRSPDFASSEFKI 189
Db 173 ILRAPDFLSTFHI 185

RESULT 4
US-10-109-885-3
; Sequence 3, Application US/10109885
; Patent No. US20020119129A1
; GENERAL INFORMATION:
; APPLICANT: REVEL, Michel
; APPLICANT: CHEBATH, Judith
; APPLICANT: ABRAMOVITCH, Carolina
; TITLE OF INVENTION: NOVEL IFN RECEPTOR I BINDING PROTEIN, DNA ENCODING THEM, AND M
; TITLE OF INVENTION: MODULATING CELLULAR RESPONSE TO INTERFERON
; FILE REFERENCE: REVEL-14A
; CURRENT APPLICATION NUMBER: US/10/109,885
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: US/09/341,640
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: PCT/US98/00671
; PRIOR FILING DATE: 1998-01-15
; PRIOR APPLICATION NUMBER: US 60/035,636
; PRIOR FILING DATE: 1997-01-15
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-10-109-885-3

Query Match 19.2%; Score 183.5; DB 12; Length 170;
Best Local Similarity 31.1%; Pred. No. 1.7e-11;
Matches 38; Conservative 31; Mismatches 48; Indels 5; Gaps 2;
QY 56 EQILSLPELKANPFKERICRVFSTSPAKDSLSFEDFLDLSVFSDTATPDIKSHYAFRIE 115
Db 41 EEFMSLPELQONPLVQRVIDIFDTD-GNGEVDFKEFIEGVSVKGDKEQKLRFAFRIY 99
QY 116 DFDDDGTLNREXLSRLVNCLTGEGEDTRLSASEMKQLIDNILEESDIDRDGTINLSEFQHV 175
Db 100 DMDKDGYSINGELFQVLKMMVG---NNLKDTQLQIYDKTIINADKDGGRISFEFCA 155
QY 176 VI 177
Db 156 VV 157

RESULT 5
US-09-999-602-3
; Sequence 3, Application US/09999602
; Patent No. US20020091084A1
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti G.
; APPLICANT: Corley, Neil C.
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: HUMAN CALCIUM BINDING PROTEIN
; FILE REFERENCE: PF-0468-2 CON


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; EARLIER FILING DATE: 1998-11-20
; EARLIER APPLICATION NUMBER: USSN 09/298,731
; EARLIER FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 216
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-350-874-6

Query Match      14.1%; Score 135; DB 10; Length 216;
Best Local Similarity 25.6%; Pred. No. 1.9e-06;
Matches 43; Conservative 34; Mismatches 77; Indels 14; Gaps 5;

QY 11 ELLAEYQDLTFLTKQEILLAHRRFCBLLPQEQRTVSSSLRAQVPFEQILS--LPCLKANP 68
| | : : | | | : : | | : : | | : : | | : : | | : : | | : : | | : :
Db 37 EGLEQLEAQTNFTKRELQVLYRGFKNECP-----SGVVNEETFQKIYAQFFPHGDAST 89
| | : : | | | : : | | : : | | : : | | : : | | : : | | : : | | : :

QY 69 FKERICRVFSTSPAKDSLSFEDFLDLLSVFSDTATPDIKSHYAFRIFDFFDDGTLNREXL 128
: : : : | | : : | | : : | | : : | | : : | | : : | | : : | | : :
Db 90 YAHYLFNAFDTTQT-GSVKFEDEVFALSILL-RGTVHEKLRWTFNLYDINKDGYINKEEM 147

QY 129 SRLVNC---LTGEGEDTRLSASEMKQLIDNILEESDIDRDGTINLSEF 173
: | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : :
Db 148 MDIVKAIYDMGKYTPVLKEDTPRQHVVDVFFQKMDKNKDGIVTLDEF 195

RESULT 9
US-09-350-874-24
; Sequence 24, Application US/09350874
; Patent No. US20020019020A1
; GENERAL INFORMATION:
; APPLICANT: Rhodes, Kenneth
; APPLICANT: An, Wenqian
; TITLE OF INVENTION: METHODS FOR TREATING CARDIOVASCULAR DISORDERS
; FILE REFERENCE: MNI-069
; CURRENT APPLICATION NUMBER: US/09/350,874
; CURRENT FILING DATE: 1999-07-09
; EARLIER APPLICATION NUMBER: USSN 60/110,277
; EARLIER FILING DATE: 1998-11-30
; EARLIER APPLICATION NUMBER: USSN 60/110,033
; EARLIER FILING DATE: 1998-11-25
; EARLIER APPLICATION NUMBER: USSN 60/109,333
; EARLIER FILING DATE: 1998-11-20
; EARLIER APPLICATION NUMBER: USSN 09/298,731
; EARLIER FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-350-874-24

Query Match      14.1%; Score 135; DB 10; Length 220;
Best Local Similarity 22.8%; Pred. No. 2e-06;
Matches 42; Conservative 46; Mismatches 82; Indels 14; Gaps 5;

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| | : : | | | : : | | : : | | : : | | : : | | : : | | : : | | : :
Db 41 EGLEQLEQTKFTRKELQVLYRGFKNECP-----SGIVNEENFKIYSQFFQGSST 93
| | : : | | | : : | | : : | | : : | | : : | | : : | | : : | | : :

QY 69 FKERICRVFSTSPAKDSLSFEDFLDLLSVFSDTATPDIKSHYAFRIFDFFDDGTLNREXL 128
: : : : | | : : | | : : | | : : | | : : | | : : | | : : | | : :
Db 94 YATFLFNAFDTN-HDGSVSFDFVAGLSVIL-RGTVDRLNWAFLNLYDLNKGDCITKEEM 151

QY 129 SRLVNC---LTGEGEDTRLSASEMKQLIDNILEESDIDRDGTINLSEFQHVISRSPDFAS 185
: : : : | | : : | | : : | | : : | | : : | | : : | | : : | | : :
Db 152 LDIMKSYDMGKYTPALREAPREHVESFFQKMDRKNKDGWVTIEEFIESCQKDNIMR 211

QY 186 SFKI 189
| : :
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Db 212 SMQL 215

RESULT 10
US-09-350-874-8
; Sequence 8, Application US/09350874
; Patent No. US20020019020A1
; GENERAL INFORMATION:
; APPLICANT: Rhodes, Kenneth
; APPLICANT: An, Wenqian
; TITLE OF INVENTION: METHODS FOR TREATING CARDIOVASCULAR DISORDERS
; FILE REFERENCE: MNI-069
; CURRENT APPLICATION NUMBER: US/09/350,874
; CURRENT FILING DATE: 1999-07-09
; EARLIER APPLICATION NUMBER: USSN 60/110,277
; EARLIER FILING DATE: 1998-11-30
; EARLIER APPLICATION NUMBER: USSN 60/110,033
; EARLIER FILING DATE: 1998-11-25
; EARLIER APPLICATION NUMBER: USSN 60/109,333
; EARLIER FILING DATE: 1998-11-20
; EARLIER APPLICATION NUMBER: USSN 09/298,731
; EARLIER FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Rattus sp.
US-09-350-874-8

Query Match      14.1%; Score 135; DB 10; Length 227;
Best Local Similarity 25.6%; Pred. No. 2.1e-06;
Matches 43; Conservative 34; Mismatches 77; Indels 14; Gaps 5;

QY 11 ELLAEYQDLTFLTKQEILLAHRRFCCELLPQEQRTVSSSLRAQVPFEQILS--LPCLKANP 68
| | : : | | | : : | | : : | | : : | | : : | | : : | | : : | | : :
Db 48 EGLEQLEAQTNFTKRELQVLYRGFKNECP-----SGVVNEETFQKIYAQFFPHGDAST 100
| | : : | | | : : | | : : | | : : | | : : | | : : | | : : | | : :

QY 69 FKERICRVFSTSPAKDSLSFEDFLDLLSVFSDTATPDIKSHYAFRIFDFFDDGTLNREXL 128
: : : : | | : : | | : : | | : : | | : : | | : : | | : : | | : :
Db 101 YAHYLFNAFDTTQT-GSVKFEDEVFALSILL-RGTVHEKLRWTFNLYDINKDGYINKEEM 158

QY 129 SRLVNC---LTGEGEDTRLSASEMKQLIDNILEESDIDRDGTINLSEF 173
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Db 159 MDIVKAIYDMGKYTPVLKEDTPRQHVVDVFFQKMDKNKDGIVTLDEF 206

RESULT 11
US-09-350-874-10
; Sequence 10, Application US/09350874
; Patent No. US20020019020A1
; GENERAL INFORMATION:
; APPLICANT: Rhodes, Kenneth
; APPLICANT: An, Wenqian
; TITLE OF INVENTION: METHODS FOR TREATING CARDIOVASCULAR DISORDERS
; FILE REFERENCE: MNI-069
; CURRENT APPLICATION NUMBER: US/09/350,874
; CURRENT FILING DATE: 1999-07-09
; EARLIER APPLICATION NUMBER: USSN 60/110,277
; EARLIER FILING DATE: 1998-11-30
; EARLIER APPLICATION NUMBER: USSN 60/110,033
; EARLIER FILING DATE: 1998-11-25
; EARLIER APPLICATION NUMBER: USSN 60/109,333
; EARLIER FILING DATE: 1998-11-20
; EARLIER APPLICATION NUMBER: USSN 09/298,731
; EARLIER FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-350-874-10
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RESULT 12
US-09-350-874-4
; Sequence 4, Application US/09350874
; Patent No. US20020019020A1
; GENERAL INFORMATION:
; APPLICANT: Rhodes, Kenneth
; APPLICANT: An, Wenqian
; TITLE OF INVENTION: METHODS FOR TREATING CARDIOVASCULAR DISORDERS
; FILE REFERENCE: MNI-069
; CURRENT APPLICATION NUMBER: US/09/350, 874
; CURRENT FILING DATE: 1999-07-09
; EARLIER APPLICATION NUMBER: USSN 60/110,277
; EARLIER FILING DATE: 1998-11-30
; EARLIER APPLICATION NUMBER: USSN 60/110,033
; EARLIER FILING DATE: 1998-11-25
; EARLIER APPLICATION NUMBER: USSN 60/109,333
; EARLIER FILING DATE: 1998-11-20
; EARLIER APPLICATION NUMBER: USSN 09/298,731
; EARLIER FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 4
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Rattus sp.
US-09-350-874-4

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RESULT 13
US-09-350-874-20
; Sequence 20, Application US/09350874
; Patent No. US20020019020A1
; GENERAL INFORMATION:
; APPLICANT: Rhodes, Kenneth
; APPLICANT: An, Wenqian
; TITLE OF INVENTION: METHODS FOR TREATING CARDIOVASCULAR DISORDERS
; FILE REFERENCE: NMT-069
; CURRENT APPLICATION NUMBER: US/09/350, 874
; CURRENT FILING DATE: 1999-07-09

Query Match	14.1%;	Score 135;	DB 10;	Length 252;
Best Local Similarity	22.8%;	Pred. No. 2.4e-06;		
Matches 42;	Conservative 46;	Mismatches 82;	Indels 14;	Gaps 5;

Db 244 SMOL 247

US-09-350-874-14

QY 69 EKERCVSTSPAKDSLSEFDLDSLVSFSDTATPDIKSHYAFRIEFDDEDDGTLNREXL 128

Db 144 YATFLNADTN-HDGSVSFEDFVAGLSVIL-RGTVDDRNLNWAFLNLYDLNKGCGITKEEM 201
QY 129 SRLVNC---LTGEGEDTRLASSEMQLIDNILEESDIDRDGTINLSEFQHVISRSPDFAS 185
Db 202 LDIMKSIYDMGKYTPALREAPREHVESFFQKMDRNKDGVVTTIEFIESCQKDENIMR 261
QY 186 SFKI 189
Db 262 SMO 265

RESULT 15

US-09-965-528-15
; Sequence 15, Application US/09965528
; Publication No. US20020187523A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: TANG, Y. Tom
; APPLICANT: YUE, Henry
; APPLICANT: LAL, Preeti
; APPLICANT: BURFORD, Neil
; APPLICANT: BANDMAN, Olga
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: AZIMZAI, Yalda
; APPLICANT: LU, Dying Aina M.
; APPLICANT: PATTERSON, Chandra
; TITLE OF INVENTION: EXTRACELLULAR SIGNALING MOLECULES
; FILE REFERENCE: PF-0701 USA
; CURRENT APPLICATION NUMBER: US/09/965,528
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/134,949
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 60/144,270
; PRIOR FILING DATE: 1999-07-15
; PRIOR APPLICATION NUMBER: 60/146,700
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: 60/157,508
; PRIOR FILING DATE: 1999-10-04
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PERL Program
; SEQ ID NO 15
; LENGTH: 216
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20020187523A1 3216587CD1
US-09-965-528-15

Query Match 14.0%; Score 134; DB 9; Length 216;
Best Local Similarity 25.6%; Pred. No. 2.4e-06;
Matches 43; Conservative 34; Mismatches 77; Indels 14; Gaps 5;
QY 11 ELLAEYQDLTFLTKQEILLAHRRFCELLPQEQRTVESLRAQVPFEQILS--LPELKANP 68
Db 37 EGLEQLEAQTNFTKRELQVLYRGFKNECP-----SGVVNEDTFKQIYAQFFPHGDAST 89
QY 69 FKERICRVFTSPAKDSLSFEDFLDLSVFSDTATPDIKSHYAFRIFDFFDDGTLNREXL 128
Db 90 YAHYLFNADFTTQT-GSVKFEDEFVLTALSILL-RGTVHEKLRWTFNLYDINKDGYINKKEEM 147
QY 129 SRLVNC---LTGEGEDTRLASSEMQLIDNILEESDIDRDGTINLSEF 173
Db 148 MDIVKAIYDMGKYTPVLKEDTPRQHVDFVFFQKMDKNKDGIVTLDEF 195

Search completed: January 17, 2003, 12:44:48
Job time : 11 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 17, 2003, 12:42:04 ; Search time 30 Seconds
(without alignments)
1311.833 Million cell updates/sec

Title: MUT127
Perfect score: 957
Sequence: 1 MGGSGSRLSKELLAERYODLT.....EFQHVISRSPDFASSFKIVL 191

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : SPTREMBL_21:*
- 1: sp_archaea:*
 - 2: sp_bacteria:*
 - 3: sp_fungi:*
 - 4: sp_human:*
 - 5: sp_invertebrate:*
 - 6: sp_mammal:*
 - 7: sp_mhc:*
 - 8: sp_organelle:*
 - 9: sp_phage:*
 - 10: sp_plant:*
 - 11: sp_rodent:*
 - 12: sp_virus:*
 - 13: sp_vertebrate:*
 - 14: sp_unclassified:*
 - 15: sp_virus:*
 - 16: sp_bacteriap:*
 - 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	406	42.4	311	5 Q93640	Q93640 caenorhabd1
2	362	37.8	185	11 Q9D9N5	Q9d9n5 mus musculi
3	339	35.4	187	4 Q96Q77	Q96q77 homo sapien
4	337.5	35.3	206	5 Q9W2Q5	Q9w2q5 drosophila
5	270	28.2	54	6 Q9GLJ2	Q9glj2 sus scrofa
6	224.5	23.5	180	5 Q9GP83	Q9gp83 dictyosteli
7	199	20.8	175	5 Q9U0X7	Q9u0x7 leishmania
8	187	19.5	175	10 Q9LS47	Q9ls47 arabidopsis
9	186	19.4	175	10 Q93VF2	Q93vf2 eucalyptus
10	181.5	19.0	169	5 Q9NEN1	Q9nfn1 schistosoma
11	180.5	18.9	244	5 Q20804	Q20804 caenorhabd1
12	179.5	18.8	189	5 Q9VNF9	Q9vnf9 drosophila
13	177.5	18.5	170	5 Q9NKM7	Q9nkw7 patinopecte
14	177.5	18.5	170	5 Q9SP81	Q9sp81 bombyx mori
15	176	18.4	200	5 Q8SRF8	Q8srf8 encephalito
16	174.5	18.2	115	11 Q99LO9	Q99lq9 mus musculu

17	173.5	18.1	187	5 Q9VWX8	Q9vwx8 drosophila
18	168.5	17.6	175	3 Q9HDE1	Q9hdel cryptococcu
19	168.5	17.6	177	3 Q9HDD3	Q9hdd3 cryptococcu
20	168	17.6	274	3 Q9AWW4	Q9aww4 oryza sativ
21	167.5	17.5	195	5 Q23643	Q23643 caenorhabd1
22	167.5	17.5	213	5 Q16343	Q16343 caenorhabd1
23	167.5	17.5	213	10 Q9L7B8	Q9l7b8 arabidopsis
24	167	17.5	170	4 Q8WYJ4	Q8wyj4 homo sapien
25	167	17.5	173	4 Q96L23	Q96l23 homo sapien
26	167	17.5	190	5 Q9NAY9	Q9nay9 naegleria f
27	162.5	17.0	161	10 Q9AY39	Q9ay39 oryza sativ
28	161.5	16.9	226	10 Q81446	Q81446 arabidopsis
29	156	16.3	190	3 Q96X50	Q96x50 magnaporthe
30	156	16.3	190	3 Q8TGC0	Q8tgc0 magnaporthe
31	151	15.8	196	5 Q9N2Y1	Q9n2y1 caenorhabd1
32	151	15.8	225	10 Q8W5C8	Q8w5c8 oryza sativ
33	149.5	15.6	226	10 Q81447	Q81447 arabidopsis
34	148.5	15.5	213	10 Q81445	Q81445 arabidopsis
35	148	15.5	246	10 Q82641	Q82641 arabidopsis
36	145	15.2	192	10 Q81328	Q81328 arabidopsis
37	145	15.2	222	10 Q81223	Q81223 arabidopsis
38	143	14.9	191	4 Q9UM19	Q9um19 homo sapien
39	140	14.6	29	11 Q99JY5	Q99jy5 mus musculu
40	139.5	14.6	153	5 Q9U5J0	Q9u5j0 trichomonas
41	139.5	14.6	160	5 Q9U5I9	Q9u5i9 trichomonas
42	135	14.1	216	11 Q9J57	Q9j57 mus musculu
43	135	14.1	220	4 Q9NS60	Q9ns60 homo sapien
44	135	14.1	220	4 Q9HD11	Q9hd11 homo sapien
45	135	14.1	220	11 Q9JM60	Q9jm60 rattus norv

ALIGNMENTS

RESULT 1	ID	Q93640	PRELIMINARY;	PRT;	311 AA.
AC	Q93640;	01-FEB-1997 (TREMBLrel. 02, Created)			
DT	01-FEB-1997 (TREMBLrel. 02, Last sequence update)				
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)				
DE	F30A10.1 protein.				
GN	F30A10.1.				
OS	Caenorhabditis elegans.				
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;				
OC	Rhabditidae; Peloderinae; Caenorhabditis.				
OX	NCBI_TaxID-6239;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	Barlow K.				
RL	Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE-99069613; PubMed-9851916;				
RA	none;				
RT	"Genome sequence of the nematode C.elegans: A platform for				
RT	investigating biology."				
RL	Science 282:2012-2018(1998).				
DR	EMBL; Z81072; CAB03019.1; .				
DR	HSSP; Q99828; 1DGv.				
DR	InterPro; IPR002048; EF-hand.				
DR	Pfam; PF00036; efhand; 3.				
DR	Prodom; PD000012; EF-hand; 1.				
DR	SMART; SM00054; EFh; 2.				
SO	SEQUENCE 311 AA; 35960 MW; 97AF0AF56A6F526F CRC64;				
QY	1 MGGSGSRLS-----KELLAERYODLTFLFKQETILAHRRFCCLLPQEQRYESS 48				
Db	111 MGNVASSLSLNLFSKGVFTREQDDEYODCTFFTRKDLIRLYKRYALNPHK---VPTN 167				

RC STRAIN-BERKELEY;
 RX MEDLINE-20196006; PubMed-10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazek R.G., Champe C.R., Miklos G.L.G.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt J.G., Nelson C.R., Pfeiffer B.D.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotler P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
 RA Fosler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kenison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Murny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 DR EMBL: AE003452; AAF46635.1; -.
 DR HSSP: Q99828; 1DGV.
 DR FlyBase: FBgn0034558; CG9236.
 DR InterPro: IPR002048; EF-hand.
 DR Pfam: PF00036; efhand; 3.
 DR ProDom: PD000012; EF-hand; 1.
 DR SMART: SM00054; EFh; 3.
 DR PROSITE: PS00018; EF_HAND; 2.
 KW Calcium-binding.
 SEQ SEQUENCE 206 AA; 23591 MW; B3105F7E70F475A9 CRC64;.

[illegible]

DT 01-MAR-2001 (TREMBLrel. 16, last sequence update)
DE 01-JUN-2002 (TREMBLrel. 21, last annotation update)
DR DNA-PK interaction-like protein (Fragment).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Smith T.P.L., Fahrenkrug S.C., Rohrer G.A., Stammen F.A.,
RA Rexroad C.E. III, Keele J.W.;
RT "Mapping of Expressed Sequence Tags from a porcine early embryonic
RT cDNA library."
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF267715; AAC25931.1; -.
DR HSSP; Q99828; 1DGV.
DR InterPro; IPR002048; EF-hand.
DR Pfam; PF00036; ehand; 1.
DR ProDom; PD000012; EF-hand; 1.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
FT NON_TER 1 1
FT NON_TER 54 54
SQ SEQUENCE 54 AA; 6107 MW; 1A8057DE68A57A4A CRC64;

	Query Match	28.2%;	Score 270;	DB 6;	Length 54;
	Best Local Similarity	96.3%;	Pred. No. 1.9e-17;		
	Matches	52;	Conservative	1;	Mismatches 1; Indels 0; Gaps 0;
OY	102	ATPDIKSHYAFRIFDDDDGTTLNRKXLSRLVNLCTGEGEPTRLSASEMKOLIDN	155		
Db	1	ATPDIKSHYAFRIFDDDDGTTLNRKEDLSQLVNLCTGEGEPTRLSASEMKOLIDN	54		

```

RESULT 6
O9GP83
ID O9GP83 PRELIMINARY; PRT; 180 AA.
AC O9GP83;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-JUN-2001 (TREMBLrel. 17, last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, last annotation update)
DE Calcineurin B.
GN CNBA.
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyostellida; Dictyostelium.
OX NCBI_TaxID=44689;
[1]
RN RP SEQUENCE FROM N.A.
RC STRAIN=AX-2;
RA Alchem A.;
RL Thesis (2000), Department of Fachbereich Biologie,
RL Universitaet Konstanz, Konstanz, Germany.
[2]
RN RP SEQUENCE FROM N.A.
RC STRAIN=AX-2;
RA Alchem A.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ301668; CAC20026.2; -.
DR HSSP; P06705; LAUI.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR001125; Recoverin.
DR Pfam; PF00036; ehand; 4.
DR PRINTS; PR00450; RECOVERIN.
DR ProDom; PD000012; EF-hand; 2.
DR SMART; SM00054; EFh; 4.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_3.
SQ SEQUENCE 180 AA; 20739 MW; E2E947E8D280D0B6 CRC64;

```

Query Match	23.5%;	Score 224.5;	DB 5;	Length 180;
Best Local Similarity	29.8%;	Pred. No. 1.2e-12;		
Matches 53;	Conservative 43;	Mismatches 67;	Indels 15;	Gaps 4;
QY	1	MGSGSRLSKELLA EYODLFTFLTKQEIILAHRRFCCLLPQEQRTVSSLRQVPFEQITLS	60	
		: : : : : : :	: : :	

Db 1 MGNQHSLLNKEQLEQMKDNSSFSEAEKLYRRFQMLDKDGSGLTIT-----DEFLS 52

QY 61 LPPELKANPFKERICRVFSTSPAKDS-LSFEDEFLLDSVFSDFATPDIKSHYAFRIFFD 119

Db 53 IPDLALNPLLRVIQFDQN--KONEIEPSEFVGTATLSHGKTKEDKLFQIYDIDC 110

QY 120 DGTNLNREXLSRLVNLCTGEGEDTRLSASEMKQLIDNILEESDIDRDGTINLSEFQHV 177

Db 111 DGFISNGELFQVLMKMGV---TNLNDVQLQIIVDKTIIEGDIYDKDKGKISDFEHI 164

RESULT 7

Q9U0X7 PRELIMINARY; PRT; 175 AA.

AC Q9U0X7

DT 01-MAY-2000 (TREMBlrel. 13, Created)

DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)

DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)

DE Calcineurin subunit.

GN L7171.06.

OS Leishmania major.

OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.

OX NCBI_TaxID=5664;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=FRIEDLIN;

RA Tosato V., Bruschi C.V., Ivens A.C., Murphy L., Quail M.,

RA Rajandream M.A., Barrell B.G.;

RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=FRIEDLIN;

RX MEDLINE=98146435; PubMed=9477341;

RA Ivens A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M.,

RA Smith D.F.;

RT "A physical map of the Leishmania major Friedlin genome.";

RL Genome Res. 8:135-145(1998).

DR EMBL; AL133435; CAB62809.1; -.

DR HSSP; P06705; 1AUI.

DR InterPro; IPR002048; EF-hand.

DR InterPro; IPR001125; Recoverin.

DR Pfam; PF00036; ehand; 4.

DR PRINTS; PR00450; RECOVERIN.

DR ProDom; PD000012; EF-hand; 2.

DR SMART; SM00054; EFh; 3.

DR PROSITE; PS00018; EF_HAND; UNKNOWN_2.

SQ SEQUENCE 175 AA; 19660 MW; 9448F127F4DFA0EB CRC64;

Query Match 20.8%; Score 199; DB 5; Length 175;

Best Local Similarity 25.3%; Pred. No. 2.3e-10;

Matches 46; Conservative 44; Mismatches 78; Indels 14; Gaps 4;

QY 8 LSKELLAEQDLTFLTKQEILLAHRRFCELLPQEQRTVLESSLRAQVPFEQILSLPEL 67

Db 6 LTAEELQNIRESALTDAQVRLYKSPSKL-----NKDKSGKITRAEFNSIPALAS 57

QY 68 PFKERICRVFSTSPAKDSLSFEDEFLLDSVFSDFATPDIKSHYAFRIFFD 127

Db 58 PLVDRVLAVMDTD-GDSTVDFGDFVRALAVLSSATSKEDKLRFTFKMYDVGDDGRIS 116

QY 128 LSRLVNLCTGEGEDTRLSASEMKQLIDNILEESDIDRDGTINLSEFQHVSRPDPASS 187

Db 117 LFQMLSIMVG---VNLSQLQIIVDKTIIEADVDVDGTYITFEFQ-ALAVNSDFGDR 171

QY 188 KI 189

Db 172 NL 173

RESULT 8

Q9LS47 PRELIMINARY; PRT; 175 AA.

ID Q9LS47

AC Q9LS47;

DT 01-OCT-2000 (TREMBlrel. 15, Created)

DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)

DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)

DE Calcineurin b subunit (Protein phosphatase 2b regulatory subunit)-like protein (Hypothetical 20.0 kDa protein).

GN AT3G18430.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.

OX NCBI_TaxID=3702;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=COLUMBIA;

RA Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata S.;

RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=COLUMBIA;

RX MEDLINE=20277480; PubMed=10819329;

RA Nakamura Y.;

RT "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence features of the regions of 4,504,864 bp covered by sixty P1 and TAC clones.";

RL DNA Res. 7:131-135(2000).

RN [3]

RP SEQUENCE FROM N.A.

RA Yamada K., Banh J., Banno F., Chang E., Dale J.M., Goldsmith A.D.,

RA Lee J.M., Onodera C.S., Quach H.L., Tang C., Toriumi M., Wu H.C.,

RA Yamamura Y., Yu G., Yu S., Bowser L., Carninci P., Chen H., Cheuk R.,

RA Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,

RA Kawai J., Kim C., Koesema E., Lam B., Lin J., Meyers M.C., Miranda M.,

RA Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M.,

RA Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,

RA Theologis A.;

RT "Full Length cDNA of gene At3g18430 (GI:15229640).";

RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.

RN [4]

RP SEQUENCE FROM N.A.

RA Yamada K., Banh J., Chan M.M., Chang C.H., Chang E., Dale J.M.,

RA Deng J.M., Goldsmith A.D., Lee J.M., Onodera C.S., Quach H.L.,

RA Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bowser L.,

RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,

RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,

RA Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J.,

RA Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Shinozaki K.,

RA Davis R.W., Ecker J.R., Theologis A.;

RT "Arabidopsis Open Reading Frame (ORF) Clones.";

RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AB026658; BAB01109.1; -.

DR EMBL; AY063789; AAL36096.1; -.

DR EMBL; AY091287; AAM14226.1; -.

DR HSSP; P06705; 1AUI.

DR InterPro; IPR002048; EF-hand.

DR Pfam; PF00036; ehand; 2.

DR ProDom; PD000012; EF-hand; 1.

DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.

KW Hypothetical protein.

SQ SEQUENCE 175 AA; 20032 MW; B26D6F2ADA26AFED CRC64;

Query Match 19.5%; Score 187; DB 10; Length 175;

Best Local Similarity 26.6%; Pred. No. 2.8e-09;

Matches 49; Conservative 45; Mismatches 66; Indels 24; Gaps 5;

QY 1 MGGSGSRLSKELLAEQYQ---DLTFLTKQEILLAHRRFCELLPQEQRTVLESSLRAQVPFE 56

Db 1 MGNTSSMLTYDIEEVQSHCHDL--FEQEIILSLYQRFQCL-----DRNAKGFI 50

QY 57 QILSLPELKANPFKERICRVFSTSPAKDSLSFEDEFLLDSVFSDFATPDIKSHYAFRI 116

Db 51 EFLSVPEFAMNPLSQRLMKV-----DGLNFKDFVAFLSAFSAKSLRQKVLIFK 104

QY 117 FDDGDTLNREXLSRLVNLCTGEGEDTRLSASEMKQLIDNILEESDIDRDGTINLSEFQHV 176

Db 105 SDCNGKVSFKDIMEVLRLDLSG-----SFMSEQREQVLSQVLKESGYTSDSFLTLEDFIKI 160
QY 177 ISRS 180
Db 161 EGSS 164

RESULT 9

093VF2. PRELIMINARY; PRT; 175 AA.
ID 093VF2
AC 093VF2
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Calcineurin-like protein.
GN ECCBL1 OR EGCB1.
OS Eucalyptus camaldulensis (Murray red gum), and
OS Eucalyptus grandis.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Myrtales; Myrtaceae; Eucalyptus.
OX NCBI_TaxID-34316, 71139;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES-E.camaldulensis, and E.grandis; TISSUE-FLOWER;
RA Fairbairn D.J., Gomez-Gallego S., Sawbridge T., Teasdale R.D.;
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF197334; AAL25650.1;
DR EMBL; AF197330; AAL25647.1;
DR InterPro; IPR002048; EF-hand.
DR Pfam; PF00036; efhand; 2.
DR ProDom; PD000012; EF-hand; 1.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
SQ SEQUENCE 175 AA; 19997 MW; C4E773EE42A3EF16 CRC64;

Query Match 19.4%; Score 186; DB 10; Length 175;
Best Local Similarity 25.8%; Pred. No. 3.5e-09;
Matches 47; Conservative 45; Mismatches 70; Indels 20; Gaps 4;

QY 1 MCGSGSRLSKELLAEQD--LFLTKQELLLAHRFCCELLPQEQRTVESSLRAQVPFEQI 58
Db 1 MGNASSMLTQYDIEEVQDHCHNLFSSQOEIVSLYERFCQL-----DRNAKGFIADDF 52
QY 59 LSLPELKANPFKERICRVSTSPAKDSLSEDFDLDSVSDTATPDIKSHYAFRIFFD 118
Db 53 LSVPEFAMNPLSQRLTKM-----DGLNFKDFVAFLSAFSAKASKQOKIELIFKVDSD 106
QY 119 DGGTLNREXLSRLVNCLTGEGEDTRLASASEMKQLIDNILEESDIDRDGTINLSEFQHVIS 178
Db 107 CNGKVSFNDILEVLRLDLSG----FMSDEQREQVLVQVLKACGYTRESYLLDDFVKVFG 162
QY 179 RS 180
Db 163 NS 164

RESULT 10

09NFN1 PRELIMINARY; PRT; 169 AA.
ID 09NFN1
AC 09NFN1
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Calcineurin B.
OS Schistosoma mansoni (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigoidida;
OC Schistosomatoida; Schistosomatidae; Schistosoma.
OX NCBI_TaxID-6183;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20520966; PubMed=11071287;
RA Mecozzi B., Rossi A., Lazzaletti P., Kady M., Kaiser S., Valle C.,

RA Clot1 D., Klinkert M.Q.;
RT "Molecular cloning of Schistosoma mansoni calcineurin subunits and
RT Immunolocalization to the excretory system."
RL Mol. Biochem. Parasitol. 110:333-343(2000).
DR EMBL; AJ276885; CAB93677.1; -.
DR HSSP; P06705; 1TCO.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR001125; Recoverin.
DR Pfam; PF00036; efhand; 4.
DR PRINTS; PR00450; RECOVERIN.
DR ProDom; PD000012; EF-hand; 2.
DR SMART; SM00054; EFh; 4.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_4.
SQ SEQUENCE 169 AA; 19137 MW; 878E01D08BC5DC1D CRC64;

Query Match 19.0%; Score 181.5; DB 5; Length 169;
Best Local Similarity 30.1%; Pred. No. 8.5e-09;
Matches 37; Conservative 31; Mismatches 50; Indels 5; Gaps 2;

QY 56 EQILSLPELKANPFKERICRVSTSPAKDSLSEDFDLDSVSDTATPDIKSHYAFRI 115
Db 40 KEFMSLPLOONPLVARVIEIFDTD-NGGEYDFKEFINGMSQFSKGEKAKLKFAFKY 98
QY 116 DFDDGTLNREXLSRLVNCLTGEGEDTRLASASEMKQLIDNILEESDIDRDGTINLSEFQH 175
Db 99 DMDKDGYSNGELFQVLKMMVG---NNLKDTQLQIVDKTIMPDKDEGRISFEFCE 154
QY 176 VIS 178
Db 155 VVS 157

RESULT 11

020804 PRELIMINARY; PRT; 244 AA.
ID 020804
AC 020804
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE F55C10.1 protein.
GN F55C10.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID-6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Dobson R.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;

RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
RT investigating biology."
RL Science 282:2012-2018(1998).
DR EMBL; Z74036; CAA98489.2; -.
DR HSSP; P06705; 1AUI.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR001125; Recoverin.
DR Pfam; PF00036; efhand; 4.
DR PRINTS; PR00450; RECOVERIN.
DR ProDom; PD000012; EF-hand; 2.
DR SMART; SM00054; EFh; 4.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_4.
SQ SEQUENCE 244 AA; 27901 MW; 6B99CB58CB77D08B CRC64;

Query Match 18.9%; Score 180.5; DB 5; Length 244;
Best Local Similarity 27.8%; Pred. No. 1.7e-08;
Matches 50; Conservative 37; Mismatches 70; Indels 23; Gaps 6;

QY 3 GSGSRLSKELLAEQD--LFLTKQELLLAHRFCCELLPQEQRTVESSLRAQVPFEQIIS 60
Db 1 GSGSRLSKELLAEQD--LFLTKQELLLAHRFCCELLPQEQRTVESSLRAQVPFEQIIS 60

Db 75 GADASLPMCMCSNFDAYELRLLT-----RRFKKL-----DVDGS--GSLSVEEFMS 118

QY 61 LPELKANPKEKICRVFSTSPAKDSLSFEDFLDLLSVFSDTATPDIKSHYAFRIFDFFDD 120

Db 119 LPELQONPLVQRVIDIFD-EDNGEVDREFIQIGISQFSVKGDKNTKLKFAFIYDMDRD 177

QY 121 GTLNREXLSRLVNLCTGEGEFTRLSASEMKQLIDNILEESIDRDGTINLSEFQHVISR 180

Db 178 GFISNGELFQVLKMMVG-----NNLKDSQLQIYDKTILFHKDGDGKISFQEFCDVVEHT 233

RESULT 12

QYVNF9

AC Q9VNF9 PRELIMINARY; PRT; 189 AA.

DT 01-MAY-2000 (TREMBlrel. 13, Created)

DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)

DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)

DE CG2185 protein (LD19356p).

GN CG2185.

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI_TaxID=7227;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-BERKELEY;

RX MEDLINE-20196006; PubMed-10731132;

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Baldwin D.,

RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Miklos G.L.G.,

RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,

RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,

RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,

RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,

RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,

RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,

RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,

RA Svirskas R., Tector C., Turner E., Venter E., Wang A.H., Wang X.,

RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,

RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,

RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,

RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;

RT "The genome sequence of Drosophila melanogaster.";

RL Science 287:2185-2195(2000).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN-BERKELEY;

RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,

RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,

RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,

RA Nunoo J., Pacleb J., Paragas V., Park S., Phouanavong S., Wan K.,

RA Yu C., Lewis S.E., Rubin G.M., Celniker S.,

RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AE003602; AAF51977.1; -

DR EMBL; AY069465; AAL39610.1; -

DR HSSP; P06705; 1AUI.

DR FlyBase; FBgn0037358; CG2185.

DR InterPro; IPR002048; EF-hand.

DR Pfam; PF00036; efhand; 2.

DR ProDom; PD000012; EF-hand; 2.

DR SMART; SM00054; EFh; 2.

DR PROSITE; PS00018; EF_HAND; 1.

KW Calcium-binding.

SQ SEQUENCE 189 AA; 21996 MW; 3621BAF72BED845D CRC64;

Query Match 18.8%; Score 179.5; DB 5; Length 189;

Best Local Similarity 25.4%; Pred. No. 1.5e-08;

Matches 48; Conservative 41; Mismatches 79; Indels 21; Gaps 4;

QY 1 MGGGSR-LSKELLAAYQDLTLTKQEILLAHRRFCELLPQEQTVESSLRAQVPFEQIL 59

Db 1 MGNKSSFLRNEEIAQIQEETGFTPNQIERLYSRFTSLDRNDCGTLRS-----EDLM 52

QY 60 SLPELKANPKEKICRVFSTSPAKDSLSFEDFLDLLSVF-----SDTATPDIKSHYA 111

Db 53 RIPELAINPLCERIVHSFFAESNDRVNFQFMVLAHFRPLRDNKQKLSNREEKLKFA 112

QY 112 FRIFDFFDDGTNLNREXLSRLVNLCTGEGEFTRLSASEMKQLIDNILEESIDRDGTINLS 171

Db 113 FKMYDLDDGVISRDELLSLHMMVG-----ANISQDLVLSIAERTILEADLCCQKISFE 168

QY 172 EFQHVISR 180

Db 169 DFCKALDRT 177

RESULT 13

QYVNF9

ID Q9NWK7 PRELIMINARY; PRT; 170 AA.

AC Q9NWK7;

DT 01-OCT-2000 (TREMBlrel. 15, Created)

DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)

DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)

DE Calcineurin B.

OS Patinopecten yessoensis (Ezo giant scallop) (Yesso scallop).

OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Pectinoida;

OC Pectinoidea; Pectinidae; Mizuhopecten.

OX NCBI_TaxID=6573;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE-TESTIS;

RA Uryu M., Nakatomi A., Watanabe M., Hatsuse R., Yazawa M.;

RT "Molecular Cloning of cDNA Encoding Two Subunits of Calcineurin from

RT Scallop Testis: Demonstration of Stage-Specific Expression during

RT Maturation of the Testis.";

RL J. Biochem. 0:0-0(2000).

DR EMBL; AB041524; BAA94543.1; -

DR HSSP; P06705; 1AUI.

DR InterPro; IPR002048; EF-hand.

DR InterPro; IPR001125; Recoverin.

DR Pfam; PF00036; efhand; 4.

DR PRINTS; PR00450; RECOVERIN.

DR ProDom; PD000012; EF-hand; 2.

DR SMART; SM00054; EFh; 4.

DR PROSITE; PS00018; EF_HAND; UNKNOWN_4.

SQ SEQUENCE 170 AA; 19238 MW; 9450322698470F44 CRC64;

Query Match 18.5%; Score 177.5; DB 5; Length 170;

Best Local Similarity 25.1%; Pred. No. 2e-08;

Matches 44; Conservative 41; Mismatches 71; Indels 19; Gaps 4;

QY 3 GSGRSLSKELLAAYQDLTLTKQEILLAHRRFCELLPQEQTVESSLRAQVPFEQILSLP 62

Db 1 : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | |

Db 2 GNENSLPMEIACSNFD-----PDEIKRLGKR-----RKLDLNSGSLSVDEFMTLP 47

QY 63 ELKANPFEKERICRVFSTSPAKDSLSFEDFLDLLSVFSDTATPDIKSHYAFRIFFDDG 122

Db 48 ELQONPLVQVIDIFD-D-GNGEVDKEFIEGVSGSVKDKLSKLRAFAFKIYDMDKDGY 106

QY 123 LNREXLSRLVNCITGEGEDTRLASSEMQLIDNILEESDIDRDGTINLSEFOHVI 177

Db 107 ISNGELFOVLKMMVG-----NNLKDTQLQOIVDKTIHADADGDKISFEFCVAV 157

RESULT 14

Q95P81 PRELIMINARY: PRT; 170 AA.

AC Q95P81; 01-DEC-2001 (Tremblrel. 19, Created)

DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)

DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)

DE Calcineurin B.

GN CNB.

OS Bombyx mori (Silk moth).

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;

OC Bombycoidea; Bombycidae; Bombyx.

OX NCBI_Taxid=7091;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=SHUKO X RYUHAKU; TISSUE=PEROMONE GLAND;

RA Yoshiga T., Matsumoto S.;

RT "CDNA cloning of heterosubunits of calcineurin from pheromone gland of Bombyx mori."

RT Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.

RL EMBL: AF287251; AAK83039.1;

DR InterPro; IPR002048; EF-hand.

DR Pfam; PF00036; efhand; 4.

DR ProDom; PD000012; EF-hand; 2.

DR PROSITE; PS00018; EF_HAND; UNKNOWN_4.

SO SEQUENCE 170 AA; 19357 MW; 5ECC15B820097130 CRC64;

Query Match 18.5%; Score 177.5; DB 5; Length 170;

Best Local Similarity 24.7%; Pred. No. 2e-08;

Matches 44; Conservative 43; Mismatches 72; Indels 19; Gaps 4;

QY 3 GSGSRLSKELLAAYQDLTLTKQELLAHRRFCCELLPQEQRTVESSLRAQVPFEQILSLP 62

Db 2 GNENSLPMEIACSNFD-----ADEIRRLGKR-----RKLDLNSGALSIDEFMSLP 47

QY 63 ELKANPFEKERICRVFSTSPAKDSLSFEDFLDLLSVFSDTATPDIKSHYAFRIFFDDG 122

Db 48 ELQONPLVQVIDIFD-ADNGEVDKEFIEGVSGSVKDKLSKLRAFAFKIYDMDKDGF 106

QY 123 LNREXLSRLVNCITGEGEDTRLASSEMQLIDNILEESDIDRDGTINLSEFOHVISRS 180

Db 107 ISNGELFOVLKMMVG-----NNLKDTQLQOIVDKTIHADKDEDKISFEFCVAVNT 160

RESULT 15

Q8SRF8 PRELIMINARY: PRT; 200 AA.

AC Q8SRF8; 01-JUN-2002 (Tremblrel. 21, Created)

DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)

DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)

DE Calcineurin beta subunit.

GN ECU08_0160.

OS Encephalitozoon cuniculi.

OC Eukaryota; Microsporidia; Unikaryonidae; Encephalitozoon.

OX NCBI_Taxid=6035;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=GB-M1;

RA Genoscope;

RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=GB-M1;

RX MEDLINE=21576510; PubMed=11719806;

RA Katinka M.D., Duprat S., Coriailot E., Metenier G., Thomarat F.,

RA Prenstier G., Barbe V., Peyretallade E., Brotlier P., Wincker P.,

RA Delbac F., El Alaoui H., Peyret P., Saurin W., Gouy M.,

RA Weissenbach J., Vivares C.P.;

RT "Genome sequence and gene compaction of the eukaryote parasite Encephalitozoon cuniculi."

RT Nature 414:450-453(2001).

RL EMBL: AL590448; CAD26322.1;

DR EMBL; AL590448; CAD26322.1;

SO SEQUENCE 200 AA; 23929 MW; 3F0A4E2910E87701 CRC64;

Query Match 18.4%; Score 176; DB 5; Length 200;

Best Local Similarity 25.9%; Pred. No. 3.3e-08;

Matches 51; Conservative 40; Mismatches 80; Indels 26; Gaps 6;

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QY 60 SLPELKANPFEKERICRVFSTSPAKDSLSFEDFLDLLSVFSDTATPDIKSHYAFRIFFDD 119

Db 53 NIPEFQSNPESHILIMKSIKMTDEKMTPEHFLFEGIFSEKNSKRNRIYLFDFIDLNG 112

QY 120 DGTINREXLSRLVNCITGEGEDTRLASSEMQLIDNILEESDIDRDGTINLSEFOHVISR 179

Db 113 DGRLCRNVLIRINKMM---GQDGRVEAE-----NLNITYDEGGKGYLDISDFTRYES 163

QY 180 SP-----DFASSFK 188

Db 164 DPLIDKMMIIDFSKNLK 180

Search completed: January 17, 2003, 12:44:32

Job time : 32 secs


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Sequence 2, Application US/09878454A
GENERAL INFORMATION:
APPLICANT: Monteiro, et al.
TITLE OF INVENTION: Method of Controlling the Binding of Calmyrin to Presenilin
FILE REFERENCE: 4115-161
CURRENT APPLICATION NUMBER: US/09/878,454A
CURRENT FILING DATE: 2001-06-11
PRIOR APPLICATION NUMBER: 60/210,939
PRIOR FILING DATE: 2000-06-11
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 191
TYPE: PRT
ORGANISM: Homo sapiens
US-09-878-454A-2x
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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 17, 2003, 12:43:19 ; Search time 36 Seconds

(without alignments)
706.969 Million cell updates/sec

Title: US-09-878-454A-2X

Perfect score: 904
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Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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Listing first 45 summaries

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23: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	875	96.8	191	19 AAW51215	Amino acid sequenc
2	869	96.1	191	19 AAW62287	Human protein phos
3	867	95.9	191	19 AAW64199	Human interferon r
4	328	36.3	172	22 AAU87324	Novel central nerv
5	328	36.3	184	22 AAM43562	Human polypeptide
6	326	36.1	185	22 AAB64418	Amino acid sequenc
7	311	34.4	173	22 ABB96054	Human testicular a
8	311	34.4	173	22 AAU87612	Novel central nerv
9	311	34.4	173	22 AAM95362	Human reproductive
10	311	34.4	173	22 AAM43637	Human polypeptide

X at p5N5 116-128

11	311	34.4	173	22 AAU19952	Novel human calcitn
12	309	34.2	187	22 AAE09736	Human kinase inter
13	297.5	32.9	206	22 ABB64325	Drosophila melanog
14	220	24.3	120	20 AAY11976	Human 5' EST secre
15	200.5	22.2	169	23 ABB41194	Human ovarian anti
16	164.5	18.2	175	20 AAY00881	Calcineurin regula
17	164	18.1	175	21 AAG21178	Calcineurin regula
18	164	18.1	210	21 AAG21177	Zea mays protein f
19	161	17.8	175	21 AAG51586	Arabidopsis thalia
20	161	17.8	175	23 ABB92357	Herbicidally activ
21	159	17.6	175	21 AAG07824	Arabidopsis thalia
22	152	16.8	169	21 AAG51587	Arabidopsis thalia
23	150	16.6	169	21 AAG07825	Arabidopsis thalia
24	150	16.6	169	21 AAG21179	Zea mays protein f
25	146.5	16.2	170	19 AAM64200	Human calcineurin
26	146.5	16.2	170	21 AAB09978	Human HCNB protein
27	133.5	14.8	162	22 ABB65554	Drosophila melanog
28	132.5	14.7	170	22 ABB60493	Arabidopsis thalia
29	130.5	14.4	226	21 AAG47032	Human CNBII protel
30	130	14.4	170	21 AAB09977	Calcineurin B subu
31	130	14.4	170	22 AA014411	Human ORFX ORF1575
32	130	14.4	173	22 AAB64410	Drosophila melanog
33	130	14.4	187	22 AAU87327	Novel central nerv
34	130	14.4	189	22 ABB95936	Human testicular a
35	130	14.4	189	22 AAU87615	Novel central nerv
36	130	14.4	189	22 AAM95239	Human reproductive
37	130	14.4	189	22 AAM43564	Human polypeptide
38	130	14.4	189	22 AAM43639	Novel human calcitn
39	130	14.4	189	22 AAU19951	Human calcineurin
40	130	14.4	214	20 AAY31625	Human colon cancer
41	130	14.4	257	22 AAG75354	Arabidopsis thalia
42	129.5	14.3	226	21 AAG21763	Human ORFX ORF1575
43	127	14.0	201	21 AAB41811	Drosophila melanog
44	126.5	14.0	187	22 ABB61857	Drosophila melanog
45	126.5	14.0	187	22 ABB67063	Drosophila melanog

ALIGNMENTS

RESULT 1
AAW51215
ID AAW51215 standard; Protein; 191 AA.

AC AAW51215;
XX
DT 21-AUG-1998 (first entry)

DE Amino acid sequence of the calcium-integrin binding protein.
XX
KW Human calcium-integrin binding protein; CIB; integrin alpha IIB;
KW cytoplasmic domain; platelet; alpha IIB-beta-3; fibrinogen receptor;
KW inhibition; blood coagulation; vascular disorder.

XX Homo sapiens.

OS
XX
FH Key
FT Region 116..128
FT /note= "EF-hand motif"
FT Region 160..173
FT /note= "EF-hand motif"

PN WO9814471-A1.
XX
PD 09-APR-1998.
XX
PF 24-SEP-1997; 97WO-US16828.
XX
PR 02-OCT-1996; 96US-0720625.
XX
PA (UYNC-) UNIV NORTH CAROLINA.
XX
PI Naik UP, Parise LV;

PN WO9831796-A1.
XX
PD 23-JUL-1998.
XX
PF 15-JAN-1998; 98WO-US00671.
XX
PR 15-JAN-1997; 97US-0035636.
XX
PA (MCIN/) MCINNIS P A.
PA (YEDA) YEDA RES & DEV CO LTD.
XX
PI Abramovitch C, Chebath JE, Revel M;
XX
DR WPI: 1998-414096/35.
DR N-PSDB: AAV44272.
XX
PT New isolated interferon receptor binding proteins - used to develop
PT products for modulating sensitivity to interferon, e.g. in the
PT treatment of tumours or for prolonging graft survival
XX
PS Claim 1; Page 34; 64pp; English.
XX
CC This is a novel human protein, designated interferon receptor
CC binding protein 1 (IRIB1), which interacts with the intracytoplasmic
CC (IC) domain of the IFNARI chain of the interferon type I (IFN-alpha,
CC beta or omega) receptor. IRIB1 is a new member of the calcineurin
CC and calcitracin family of calcium-regulated proteins (see also
CC AAW64200). It is induced very rapidly and transiently following IFN
CC treatment of human cells. It was identified in a two-hybrid
CC screening for proteins interacting with the IFNARI-IC domain;
CC another protein, IRIB4 (see AAW64202), was similarly identified. A
CC cDNA clone (see AAV44272) encoding IRIB1, host cells and expression
CC vectors are claimed. DNA encoding IRIB1 and IRIB4 can be used in
CC cancer therapy where the increased cellular response to IFN would
CC result in a decrease in malignant cell growth and an enhanced
CC response to exogenous IFN therapy. Antisense IRIB1 or IRIB4
CC nucleic acids can be used for prolonging tissue or organ graft
CC survival in patients as the rejection of these grafts in the host
CC is mediated by the histocompatibility antigens (MHC class I) whose
CC synthesis depends on the IFN stimulus. The products can also be
CC used in detection and diagnosis.
XX
SQ Sequence 191 AA;
QY 1 MGGSGSRLSKELLAQYDLFLTKQELLAHRRFCCLLPQEQRTVESSLRAQVPEQILS 60
Db 1 MGGSGSRLSKELLAQYDLFLTKQELLAHRRFCCLLPQEQRTVESSLRAQVPEQILS 60
QY 61 LPELKANPFKERICRVSTSPAKDSLSFEDFLDLVSFSDTATPDIKSHYAFRIEXXXX 120
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QY 121 XXXXXXSRLVNCLTGEGEDTRLASASEMKQLIDNILEESDIDRDGTINLSEFQHVISRS 180
Db 121 GTLNREDLSRLVNCLTGEGEDTRLASASEMKQLIDNILEESDIDRDGTINLSEFQHVISRS 180
QY 181 PDFASSFKIVL 191
Db 181 PDFASSFKIVL 191

DE Novel central nervous system protein #234.
XX
KW Central nervous system; CNS; autoimmune disease; rheumatoid arthritis;
KW hyperproliferative disorder; neoplasm; cardiovascular disorder;
KW cardiac arrest; cerebrovascular disorder; ischaemia; anglogenesis;
KW nervous system disorder; Alzheimer's disease; AIDS; ocular disorder;
KW acquired immunodeficiency virus; dysphagia; gastrointestinal disorder;
KW adenocarcinoma; reproductive system disorder; testicular feminisation;
KW endocrine disorder; diabetes; cancer; leukaemia; neovascularisation;
KW respiratory disorder; renal disorder; kidney failure; blood disorder;
KW myocardial infarction; wound healing; cell proliferation; skin aging;
KW food additive; food preservative; gene therapy.
XX
OS Homo sapiens.
XX
PN WO200155318-A2.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01332.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
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PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226868.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
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PR 06-SEP-2000; 2000US-0230438.
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PR 08-SEP-2000; 2000US-0231414.
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PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.

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KW	cerebroprotective; nootropic; neuroprotective; antibacterial; virucide;	PR	14-SEP-2000;	2000US-0233064.
KW	fungicide; ophthalmological; cytostatic; immunosuppressive; nootropic;	PR	14-SEP-2000;	2000US-0233065.
KW	neuroprotective; antiallergic; hepatotropic; antidiabetic;	PR	21-SEP-2000;	2000US-0234223.
KW	antiflammatory; antilicer; vulnerary; anticonvulsant; antibacterial;	PR	21-SEP-2000;	2000US-0234274.
KW	antiparasitic; cardiant; gene therapy; cancer; immune disorder;	PR	25-SEP-2000;	2000US-0234997.
KW	cardiovascular disorder; neurological disease; infection; human.	PR	25-SEP-2000;	2000US-0235484.
XX		PR	26-SEP-2000;	2000US-0235834.
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XX		PR	29-SEP-2000;	2000US-0236327.
PN	WO200155308-A2.	PR	29-SEP-2000;	2000US-0236367.
XX		PR	29-SEP-2000;	2000US-0236368.
PD		PR	29-SEP-2000;	2000US-0236370.
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XX		PR	17-NOV-2000;	2000US-0249208.
XX		PR	17-NOV-2000;	2000US-0249209.
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XX		PR	17-NOV-2000;	2000US-0249214.
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XX		PR	01-DEC-2000;	2000US-0250160.
XX		PR	01-DEC-2000;	2000US-0250391.
XX		PR	05-DEC-2000;	2000US-0251030.
XX		PR	05-DEC-2000;	2000US-0251988.

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PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PI
XX Rosen CA, Barash SC, Ruben SM;
XX
DR WPI; 2001-488781/53.
DR N-PSDB; AAI63868.
XX
PT New isolated nucleic acids and polypeptides, useful for diagnosing,
PT treating and/or preventing human diseases and disorders -
XX
PS Claim 11; SEQ ID NO 240; 664pp + Sequence Listing; English.
XX
PS The invention relates to human polynucleotides (AAI63803-AAI64012) and
CC the encoded proteins (AAM434497-AAM43660) useful for preventing, treating
CC or ameliorating medical conditions e.g. by protein or gene therapy. The
CC genes were isolated from a range of human tissues disclosed in the
CC specification. The nucleic acids, proteins, antibodies and (ant)agonists
CC are useful in the diagnosis, treatment and prevention of: (a) cancer,
CC e.g. breast and ovarian cancer and other cancers of the adrenal gland,
CC bone, bone marrow, breast, gastrointestinal tract, liver, lung, or
CC urogenital; (b) immune disorders e.g. Addison's disease, allergies,
CC autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus,
CC Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative
CC colitis; (c) cardiovascular disorders such as myocardial ischaemias;
CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
CC and parasitic infections.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 184 AA;

Query Match 36.3%; Score 328; DB 22; Length 184;
Best Local Similarity 40.7%; Pred. No. 1.4e-31;
Matches 72; Conservative 31; Mismatches 64; Indels 10; Gaps 3;

QY 13 LAEYQDLTFLTKQEILLAHRRFCELLPQEQRTVESSLRAQVPFEQILSLPELKANPFKE 72
Db 13 LEEYQALTFLTRNEILCIHDTFLKLCPPGKYKATL---TMDQVSSLPALRVNPFDR 68
QY 73 ICRVFTSPAKDSLSFEDFLDLLSVFSDTATPDIKSHYAFRIFXXXXXXXSRLV 132
Db 69 ICRVFS---HKGMFSFEDVLGMAVFSEQACPSLKIEYAFRIYDFNENGFIDEEDLQRII 125

QY 133 NCLTGEGETRLSASEMKQLIDNILEESDIDRDGTINLSEFQHVISRSPDFASSFKI 189
Db 126 LRLNLSDD---MSEDLMLDNLNHLVSESDLDNDNMLSFSEFEHAMAKSPDFMNSFRI 179

RESULT 6
AAB64418
ID AAB64418 standard; Protein; 185 AA.
XX
AC AAB64418;
XX
XX 22-MAR-2001 (first entry)
XX
XX Amino acid sequence of human intracellular signalling molecule INTRA50.
KW Human; intracellular signalling molecule; INTRA; immunosuppressive;
KW cytostatic; neuroprotective; nootropic; antiarteriosclerotic; cancer;
KW antiinflammatory; anti-HIV; neuroleptic; antibacterial; antifungal;
```

```
KW antiviral; antiparasitic; antihelminthic; antiparkinsonian; AIDS;
KW cell proliferative disorder; arteriosclerosis autoimmune; epilepsy;
KW inflammatory disorder; Addison's disease; gastrointestinal disorder;
KW neurological disorder; Parkinson's disease; Creutzfeldt-Jakob disease;
KW mental disorder; schizophrenia; anxiety.
XX Homo sapiens.
OS
XX WO200077040-A2.
PN
XX
PD 21-DEC-2000.
XX
XX 16-JUN-2000; 2000WO-US16636.
XX
XX 16-JUN-1999; 99US-0139566.
PR 17-AUG-1999; 99US-0149640.
PR 09-NOV-1999; 99US-0164417.
XX
XX (INCY-) INCYTE GENOMICS INC.
PA
XX Yue H, Tang YT, Hillman JL, Lal P, Bandman O, Baughn MR;
PI Azimzai Y, Yang J, Reddy R, Lu DAM;
PI
XX WPI; 2001-025334/03.
DR N-PSDB; AAF32687.
XX
XX New human intracellular signaling molecules, useful for the diagnosis,
PT prevention and treatment of cell proliferative, autoimmune,
PT inflammatory, neurological, gastrointestinal, reproductive and
PT developmental disorders -
XX
XX Claim 5; Page 158-159; 192pp; English.
PS
XX Sequences AAF32638 - AAF32689 represent cDNA encoding human
CC intracellular signalling molecules INTRAL - INTRA52, represented in
CC AAB64369 - AAB64420. Modulators of the intracellular signalling molecules
CC of the invention exhibit immunosuppressive; cytostatic; neuroprotective;
CC nootropic; antiarteriosclerotic; antiinflammatory; anti-HIV;
CC neuroleptic; antibacterial; antifungal; antiviral; antiparasitic;
CC antihelminthic; and antiparkinsonian activity. INTRA polypeptides their
CC agonists and antagonists are useful for the treatment of a condition
CC associated with decreased or increased expression of functional INTRA.
CC Disorders associated with abnormal INTRA expression or activity include
CC cell proliferative disorders e.g. arteriosclerosis and cancers;
CC autoimmune or inflammatory disorders e.g. Addison's disease and acquired
CC immunodeficiency syndrome (AIDS); viral, bacterial, fungal, parasitic,
CC protozoal and helminthic infections; gastrointestinal disorders e.g.
CC dysphagia and irritable bowel syndrome; neurological disorders e.g.
CC epilepsy and Parkinson's disease; prion diseases e.g. Creutzfeldt-Jakob
CC disease and mental disorders e.g. anxiety, schizophrenia and Tourette's
CC disorder. Antibodies immuno specific for the INTRA proteins may also be
CC useful in the diagnosis of the above disorders.
XX
SQ Sequence 185 AA;

Query Match 36.1%; Score 326; DB 22; Length 185;
Best Local Similarity 40.8%; Pred. No. 2.4e-31;
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QY 71 ERICRVFTSPAKDSLSFEDFLDLLSVFSDTATPDIKSHYAFRIFXXXXXXXSR 130
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Db 125 IILRLNLSDD---MSEDLMLDNLNHLVSESDLDNDNMLSFSEFEHAMAKSPDFMYSFRI 180

RESULT 7
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ABB96054
ID ABB96054 standard; Protein; 173 AA.
XX
AC ABB96054;
XX
DT 21-JUN-2002 (first entry)
XX
DE Human testicular antigen SEQ ID NO: 1438.
XX
KW Human; testicular antigen; testes; cancer; metastasis; immune disorder;
KW reproductive system disorder; urinary system disorder; gene therapy;
KW cardiovascular disorder; respiratory disorder; neurological disorder;
KW gastrointestinal disease; infection; cytostatic.
XX
OS Homo sapiens.
XX
PN WO200155317-A2.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01329.
XX
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PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX

PI Rosen CA, Barash SC, Ruben SM;
XX
DR WPI; 2001-581633/65.
DR N-PSDB; ABK43942.
XX
PT New isolated nucleic acid encoding a protein for diagnosing,
PT preventing, treating or ameliorating medical conditions and used as
PT food additives or preservatives .
XX
PS Claim 9; SEQ ID No 1130; 837pp; English.
XX
CC The invention describes an isolated nucleic acid molecule (I) encoding a
CC novel central nervous system protein. (I) and polypeptides (II) encoded
CC by (I), are used to treat a medical conditions and in diagnosis of a
CC pathological condition. Disorders which are diagnosed or treated include
CC autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative
CC disorders e.g. neoplasms of the breast or liver, cardiovascular disorders
CC e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia,
CC anglogenesis, nervous system disorders e.g. Alzheimer's disease and
CC amyloidrophic lateral sclerosis, infections caused by bacteria, viruses
CC e.g. Acquired immunodeficiency virus (AIDS) and fungi, ocular disorders
CC e.g. corneal infection, gastrointestinal disorders e.g. dysphagia,
CC adenocarcinomas and irritable bowel syndrome, reproductive system
CC disorders e.g. testicular feminisation, endocrine disorders e.g. diabetes
CC and pituitary dwarfism, cancers and disorders at the cellular level e.g.
CC leukaemia, disorders involving neovascularisation e.g. malignancies,
CC respiratory disorders e.g. nonallergic rhinitis, renal disorders e.g.
CC acute kidney failure and blood related disorders e.g. myocardial
CC infarction. The polypeptides can also be used to aid wound healing and
CC epithelial cell proliferation, to prevent skin aging due to sunburn, to
CC maintain organs before transplantation, for supporting cell culture of
CC primary tissues, to regenerate tissues and in chemotaxis. The
CC polypeptides can also be used as a food additive or preservative to
CC increase or decrease storage capabilities, fat content, lipid, protein,

Query Match 34.4%; Score 311; DB 22; Length 173;
Best Local Similarity 39.4%; Pred. No. 1.5e-29;
Matches 69; Conservative 30; Mismatches 66; Indels 10; Gaps 3;

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RESULT 9
AAM95362
ID AAM95362 standard; Protein; 173 AA.
XX
AC AAM95362;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human reproductive system related antigen SEQ ID NO: 4020.
XX
KW Human; reproductive system related antigen; reproductive system disorder;
XX cancer; gene therapy.
OS Homo sapiens.
XX
PN WO200155320-A2.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01339.
XX

PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
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PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.

(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Barash SC, Ruben SM;

WPI; 2001-465570/50.

N-PSDB; AAL01332.

Isolated nucleic acid molecule encoding a reproductive system antigen
is used in preventing, treating or ameliorating a medical condition


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XX PS Claim 11; SEQ ID NO 4020; 1297pp + Sequence Listing; English.
XX CC The present invention provides the protein and coding sequences of a
CC number of human reproductive system related antigens. These can be used
CC in the prevention and treatment of reproductive system disorders,
CC including cancer. The present sequence is a protein of the invention.
XX SQ Sequence 173 AA;

Query Match          34.4%; Score 311; DB 22; Length 173;
Best Local Similarity 39.4%; Pred. No. 1.5e-29;
Matches 69; Conservative 30; Mismatches 66; Indels 10; Gaps 3;

QY 13 LAEYQDLTFLTKQELLAHRRFCCELLPQEQRTVESSLRAQVPFEQILSLPELKANPEKER 72
   1 LEEYQALTFLTRNEILCIHDTFLKLCPPGKYYKEATL---TMDQVSSLPALRYNPERDR 56
   73 ICRVFSTSPAKDSLSEFEDFLDLVSFSDTAPFDIKSHYAFRIEXXXXXXXXSRLV 132
   57 ICRVFS--HKGMFSFEDVLGMASVFSQACPSLKIETAFRIYDFNENGFIDEEDLQRII 113
   133 NCLTGEGETRSLASEMKOLIDNILESDIDRDGTINLSEFQHVISRSPDFASSF 187
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Db 114 LRLNSDD---MSEDLIMDLTINHLVLSXSDLDNDMLSFSEFEHMAKSPDEMTPTF 165

RESULT 10
AAM43637
ID AAM43637 standard; Protein; 173 AA.
XX AC AAM43637;
DT 22-OCT-2001 (first entry)
XX DE Human polypeptide SEQ ID NO 315.
XX KW Human; antiarthritic; antirheumatic; antiproliferative; vasotropic;
KW cerebroprotective; nootropic; neuroprotective; antibacterial; virucide;
KW fungicide; ophthalmological; cytostatic; immunosuppressive; nootropic;
KW neuroprotective; antiallergic; hepatotropic; antidiabetic;
KW antiinflammatory; antiulcer; vulnery; anticonvulsant; antibacterial;
KW antiparasitic; cardiant; gene therapy; cancer; immune disorder;
KW cardiovascular disorder; neurological disease; infection; human.
XX OS Homo sapiens.
XX PN WO200155308-A2.
XX XX 02-AUG-2001.
XX PD 17-JAN-2001; 2001WO-US01309.
XX PF 31-JAN-2000; 2000US-0179065.
XX PR 04-FEB-2000; 2000US-0180628.
XX PR 24-FEB-2000; 2000US-0184664.
XX PR 02-MAR-2000; 2000US-0186350.
XX PR 16-MAR-2000; 2000US-0189874.
XX PR 17-MAR-2000; 2000US-0190076.
XX PR 18-APR-2000; 2000US-0198123.
XX PR 19-MAY-2000; 2000US-0205515.
XX PR 07-JUN-2000; 2000US-0209467.
XX PR 28-JUN-2000; 2000US-0214886.
XX PR 30-JUN-2000; 2000US-0215135.
XX PR 07-JUL-2000; 2000US-0216647.
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XX PR 14-AUG-2000; 2000US-0224518.
XX PR 14-AUG-2000; 2000US-0224519.
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PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.

(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Barash SC, Ruben SM;

WPI; 2001-465568/50.

N-PSDB; AAS31637.

Isolated nucleic acid molecule encoding a calcium-binding protein is used in preventing, treating or ameliorating a medical condition -
Claim 11; SEQ ID No 149; 542pp; English.

The present invention relates to the isolation of novel human calcium-binding proteins, and cDNA (AAS31577-AAS31654) and genomic sequences encoding for these proteins. The sequences of the invention are useful in the diagnosis, prevention and/or prognosis of diseases associated with aberrant calcium flux. Such disorders include neurological diseases (e.g. amyotrophic lateral sclerosis, ALS), immune dysfunction (e.g. severe combined immunodeficiency, SCID), digestive disorders (e.g. irritable bowel syndrome, IBS), neoplastic disease (e.g. cancer), blood disorders (e.g. haemophilia), and/or infectious disease (e.g. acquired immunodeficiency syndrome, AIDS). The novel calcium-binding proteins are also useful as screening tools to identify antagonists and/or agonists that may enhance or inhibit activities mediated by calcium-binding proteins. The polynucleotides of the invention are also useful in gene therapy. AAU19892-AAU19969 represent the novel human calcium-binding proteins. The polynucleotides of Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

Sequence 173 AA;

Query Match 34.4%; Score 311; DB 22; Length 173;
Best Local Similarity 39.4%; Pred. No. 1.5e-29;
Matches 69; Conservative 30; Mismatches 66; Indels 10; Gaps 3;

Db 43 KDCITFTTRKEILRVHKKRFELRPDLVPRQMTGQASSVKVPECEIEKMPELR----- 94
QY 74 CRVFSTSPAKDLSFEDFLDLISVFSDTATPDIKSHYAFRIFXKXXXXXXXSRLVN 133
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QY 134 CLTGEEDTRLASSEMKOLIDNILESDIDRDGTINLSEFQHVISRSPDFASSFKI 189
Db 150 CLTMTKN-ELSPEEHQIADKVIIEADVGDGKLSILEFEHVILRAPDFLSTFHI 204

RESULT 14
AAV11976
ID AAV11976 standard; Protein; 120 AA.
XX AAV11976;
AC AAV11976;
XX 18-JUN-1999 (first entry)
DT Human 5' EST secreted protein SEQ ID NO: 576.
XX Human; secreted protein; EST; expressed sequence tag; diagnosis;
KW forensic; gene therapy; chromosome mapping; signal peptide; prostate;
KW upstream regulatory sequence; cytokine activity; cell proliferation;
KW differentiation; haematopoiesis regulation; tissue growth regulation;
KW reproductive hormone regulation; chemotactic; chemokinetic; haemostatic;
KW thrombolytic; anti-inflammatory; tumour inhibition.
XX Homo sapiens.
OS WO9906550-A2.
XX 11-FEB-1999.
PD 31-JUL-1998; 98WO-IB01232.
XX 01-AUG-1997; 97US-0905144.
PR (GEST) GENSET.
XX Duclet A, Dumas Milne Edwards J, Lacroix B;
PI WPI; 1999-153780/13.
DR N-PSDB; AAX40698.
XX New isolated prostate-derived nucleic acids - used to develop
PT products which may have cytokine, immune regulatory, haematopoiesis
PT regulating, anti-inflammatory or tumour inhibition activity
XX Claim 34; Page 664; 675pp; English.
PS AAX40438 to AAX40715 represent 5' expressed sequence tags (ESTs) for
CC human secreted proteins expressed in prostate, and encode the proteins
CC given in AAV11716 to AAV11993 respectively. The proteins given represent
CC the signal peptide and an N-terminal fragment of a secreted protein. The
CC nucleic acid sequences can be used for producing secreted human gene
CC products. They can also be used to develop products for diagnosis and
CC therapy. The proteins obtained may have cytokine activity, cell
CC proliferation and differentiation activity, haematopoiesis regulating
CC activity, tissue growth regulating activity, reproductive hormone
CC regulating activity, chemotactic/chemokinetic activity, haemostatic and
CC thrombolytic activity, receptor/ligand activity, anti-inflammatory
CC activity, tumour inhibition activity or other activities. The products
CC can be used in forensic, gene therapy and chromosome mapping procedures.
CC The sequences can also be used for obtaining corresponding promoter
CC sequences. The nucleic acids encoding the signal peptides can be used for
CC directing extracellular secretion of a polypeptide or the insertion of a
CC polypeptide into a membrane, or importing a polypeptide into a cell.
XX Sequence 120 AA;
SQ Query Match 24.3%; Score 220; DB 20; Length 120;

Best Local Similarity 66.2%; Pred. No. 1.2e-18;
Matches 45; Conservative 4; Mismatches 19; Indels 0; Gaps 0;
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QY 61 LPELKANP 68
Db 61 FQSSRPYP 68

RESULT 15
ABP41194
ID ABP41194 standard; Protein; 169 AA.
XX ABP41194;
AC ABP41194;
XX 23-AUG-2002 (first entry)
DT Human ovarian antigen HTLHN94, SEQ ID NO:2326.
XX Human ovarian antigen HTLHN94, SEQ ID NO:2326.
KW Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
KW ovarian cancer; breast cancer; reproductive system disorder;
KW infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
KW PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection;
KW inflammatory condition; immune disorder; blood disorder;
KW cardiovascular disorder; respiratory disorder; neurological disorder;
KW gastrointestinal disorder; urinary system disorder; drug screening;
KW gene therapy; chromosome mapping; forensic analysis;
KW antibody preparation; cytostatic; immunomodulatory; neuroprotective;
KW antiinflammatory; gynaecological; reproductive.
XX Homo sapiens.
OS WO200200677-A1.
XX 03-JAN-2002.
PD 07-JUN-2001; 2001WO-US18569.
XX 07-JUN-2000; 2000US-209467P.
PR (HUMA-) HUMAN GENOME SCI INC.
XX Birse CE, Rosen CA;
PI WPI; 2002-147878/19.
DR N-PSDB; ABQ54271.
XX Isolated nucleic acid molecules encoding novel ovarian polypeptides,
PT useful in the prevention, treatment and diagnosis of cancer (e.g.
PT ovarian cancer), immune disorders, cardiovascular disorders and
PT neurological diseases -
XX Claim 11; SEQ ID NO 2326; 2922pp; English.
PS The invention relates to 2175 novel human ovarian antigens (ABP41054-
CC ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also
CC encompasses polypeptides 90% identical and polynucleotides 95% identical
CC to the sequences of the invention. The invention additionally relates to
CC recombinant vectors and host cells comprising human ovarian antigen
CC polynucleotides, antibodies against human ovarian antigens, and the use
CC of ovarian antigen polynucleotides and polypeptides in diagnosing,
CC treating, prognosing or preventing various ovary and/or breast-related
CC disorders. Such conditions include ovarian cancer and breast cancer, and
CC metastatic tumours of ovarian or breast origin, reproductive system
CC disorders (e.g., infertility, disorders of pregnancy, anovulation,
CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine
CC disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic
CC shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and
CC vaginitis), immune disorders (e.g., congenital and acquired
CC immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),

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OM protein - protein search, using sw model

Run on: January 17, 2003, 12:44:54 : Search time 14 Seconds
(without alignments)
401.413 Million cell updates/sec

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Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	875	96.8	191	4	US-08-720-625-2 Sequence 2, Appl1
2	869	96.1	191	3	US-08-764-563-1 Sequence 1, Appl1
3	176.5	19.5	177	3	US-08-764-563-3 Sequence 3, Appl1
4	164.5	18.2	174	1	US-08-328-322-17 Sequence 17, Appl1
5	153.5	17.0	157	1	US-08-328-322-15 Sequence 15, Appl1
6	146.5	16.2	169	4	US-08-720-625-4 Sequence 4, Appl1
7	146.5	16.2	170	3	US-08-764-563-5 Sequence 5, Appl1
8	130.5	14.4	179	3	US-08-764-563-4 Sequence 4, Appl1
9	126	13.9	186	3	US-08-655-352-8 Sequence 8, Appl1
10	126	13.9	186	4	US-09-258-016-8 Sequence 8, Appl1
11	126	13.9	186	4	US-09-257-825B-8 Sequence 7, Appl1
12	117	12.9	191	3	US-08-655-352-7 Sequence 7, Appl1
13	117	12.9	191	4	US-09-258-016-7 Sequence 7, Appl1
14	117	12.9	191	4	US-09-257-825B-7 Sequence 7, Appl1
15	116	12.8	193	3	US-08-655-352-3 Sequence 3, Appl1
16	116	12.8	193	4	US-09-258-016-3 Sequence 3, Appl1
17	116	12.8	193	4	US-09-257-825B-3 Sequence 3, Appl1
18	108.5	12.0	196	3	US-09-048-889-1 Sequence 1, Appl1
19	108	11.9	191	3	US-08-655-352-5 Sequence 5, Appl1
20	108	11.9	191	3	US-08-655-352-6 Sequence 5, Appl1
21	108	11.9	191	4	US-09-258-016-5 Sequence 5, Appl1
22	108	11.9	191	4	US-09-258-016-6 Sequence 5, Appl1
23	108	11.9	191	4	US-09-257-825B-5 Sequence 5, Appl1
24	108	11.9	191	4	US-09-257-825B-6 Sequence 5, Appl1
25	106	11.7	220	4	US-09-298-913-26 Sequence 26, Appl1
26	106	11.7	220	4	US-09-298-913-26 Sequence 26, Appl1
27	104	11.5	20	4	US-08-720-625-10 Sequence 10, Appl1

28	101	11.2	193	3	US-08-655-352-4 Sequence 4, Appl1
29	101	11.2	193	4	US-09-258-016-4 Sequence 4, Appl1
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31	101	11.2	220	4	US-09-298-913-24 Sequence 24, Appl1
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33	101	11.2	252	4	US-09-399-913-20 Sequence 20, Appl1
34	101	11.2	252	4	US-09-298-731-20 Sequence 20, Appl1
35	101	11.2	270	4	US-09-399-913-14 Sequence 14, Appl1
36	101	11.2	270	4	US-09-298-731-14 Sequence 14, Appl1
37	98	10.8	193	3	US-08-655-352-2 Sequence 2, Appl1
38	98	10.8	193	4	US-09-258-016-2 Sequence 2, Appl1
39	98	10.8	270	4	US-09-399-913-18 Sequence 18, Appl1
40	98	10.8	270	4	US-09-298-731-18 Sequence 18, Appl1
41	97	10.7	193	4	US-09-257-825B-2 Sequence 2, Appl1
42	96	10.6	225	4	US-09-298-913-30 Sequence 30, Appl1
43	96	10.6	225	4	US-09-298-913-30 Sequence 30, Appl1
44	96	10.6	252	4	US-09-399-913-22 Sequence 22, Appl1
45	96	10.6	252	4	US-09-399-913-28 Sequence 28, Appl1

ALIGNMENTS

RESULT 1
US-08-720-625-2
: Sequence 2, Application US/08720625.
: Patent No. 6242587
: GENERAL INFORMATION:
: APPLICANT: Naik, Ulhas P.
: APPLICANT: Parise, Leslie V.
: TITLE OF INVENTION: CALCIUM-INTEGRIN BINDING PROTEIN
: NUMBER OF SEQUENCES: 10
: CORRESPONDENCE ADDRESSES:
: ADDRESSEE: Bell, Seltzer, Park & Gibson
: STREET: P.O. Drawer 34009
: CITY: Charlotte
: STATE: No. 6242587th Carolina
: COUNTRY: USA
: ZIP: 28234
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/720,625
: FILING DATE:
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Sibley, Kenneth D.
: REGISTRATION NUMBER: 31,665
: REFERENCE/DOCKET NUMBER: 5470-138
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 919-420-2200
: TELEFAX: 919-881-3175
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 191 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-720-625-2

Query Match 96.8%; Score 875; DB 4; Length 191;
Best Local Similarity 92.7%; Pred. No. 1.9e-99;
Matches 177; Conservative 1; Mismatches 13; Indels 0; Gaps 0;

QY 1 MGSGSRLSKELLA EYQDLTFLTKQETLLAHRRCCELLPQEQRTVSSLRQVPFEQILS 60
Db 1 MGSGSRLSKELLA EYQDLTFLTKQETLLAHRRCCELLPQEQRTVSSLRQVPFEQILS 60
QY 61 LPELKNPKRERICRVFTSPAKDSLSFEDFLDLSVFSQDTATPDIKSHYAFRIFFXXXXX 120

Db 61 LPELKANPFKERICRVFSTSPAKDSLSFEDFLDLLSVFSDTATPDIKSHYAFRIFDFDDD 120
QY 121 XXXXXXXXSRVLNCLTGEGETRLSASEMKQLIDNILEESDIDRDGTINLSEFQHVISR 180
Db 121 GTLNREDLSRLVNCLTGEGETRLSASEMKQLIDNILEESDIDRDGTINLSEFQHVISR 180
QY 181 PDFASSFKIVL 191
Db 181 PDFASSFKIVL 191

RESULT 2
US-08-764-563-1
; Sequence 1, Application US/08764563
; Patent No. 6093565
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: A NOVEL PROTEIN PHOSPHATASE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/764,563
; FILING DATE: Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0178 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 191 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: Consensus
; CLONE: Consensus
US-08-764-563-1

Query Match 96.1%; Score 869; DB 3; Length 191;
Best Local Similarity 92.1%; Pred. No. 1e-98;
Matches 176; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
QY 1 MGGSGSRLSKELLAQYDLTFLTKQEILLAHRRFCELLPQEQRTVSSSLRAQVPFEQILS 60
Db 1 MGGSGSRLSKELLAQYDLTFLTKQEILLAHRRFCELLPQEQRTVSSSLRAQVPFEQILS 60
QY 61 LPELKANPFKERICRVFSTSPAKDSLSFEDFLDLLSVFSDTATPDIKSHYAFRIFXXXXX 120
Db 61 LPELKANPFKERICRVFSTSPAKDSLSFEDFLDLLSVFSDTATPDIKSHYAFRIFDFDDD 120
QY 121 XXXXXXXXSRVLNCLTGEGETRLSASEMKQLIDNILEESDIDRDGTINLSEFQHVISR 180
Db 121 GTLNREDLSRLVNCLTGEGETRLSASEMKQLIDNILEESDIDRDGTINLSEFQHVISR 180

QY 181 PDFASSFKIVL 191
Db 181 PDFASSFKIVL 191
RESULT 3
US-08-764-563-3
; Sequence 3, Application US/08764563
; Patent No. 6093565
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: A NOVEL PROTEIN PHOSPHATASE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/764,563
; FILING DATE: Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0178 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 177 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 458230
US-08-764-563-3

Query Match 19.5%; Score 176.5; DB 3; Length 177;
Best Local Similarity 26.4%; Pred. No. 8.3e-14;
Matches 47; Conservative 37; Mismatches 81; Indels 13; Gaps 3;
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Db 1 MGTNTSSRLRPEVEEMQGTNFTQKEIKLYKRFKLDKDGNGTISK-----DEFLM 52
QY 61 LPELKANPFKERICRVFSTSPAKDSLSFEDFLDLLSVFSDTATPDIKSHYAFRIFXXXXX 120
Db 53 IPELAVNPLVKRVISIFDEN-GDGSVNFKEFIAALS VFNAQGDQKQKLEFAFKYDIDGD 111
QY 121 XXXXXXXXSRVLNCLTGEGETRLSASEMKQLIDNILEESDIDRDGTINLSEFQHVISR 178
Db 112 GYISNGELFTVLKMMVG----NNLSDVQLQIYDKTILEADEDDGDKISFEFAKTL 165
RESULT 4
US-08-328-322-17
; Sequence 17, Application US/08328322


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; Patent No. 5723436
; GENERAL INFORMATION:
; APPLICANT: Huang, Laiqiang
; APPLICANT: Cyert, Martha S.
; TITLE OF INVENTION: Calcineurin Interacting Protein Compositions
; TITLE OF INVENTION: and Methods
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
;
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/328,322
; FILING DATE: 24-OCT-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Sholtz, Charles K.
; REGISTRATION NUMBER: P38,615
; REFERENCE/DOCKET NUMBER: 8600-0151.10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 174 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
; US-08-328-322-17

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/328,322
;   FILING DATE: 24-OCT-1994
;   CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
;   NAME: Sholtz, Charles K.
;   REGISTRATION NUMBER: P38,615
; REFERENCE/DOCKET NUMBER: 8600-0151.10
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (415) 324-0880
;   TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 157 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-328-322-15

Query Match      17.0%; Score 153.5; DB 1; Length 157;
Best Local Similarity 24.0%; Pred. No. 4.6e-11;
Matches 37; Conservative 37; Mismatches 67; Indels 13; Gaps 3;

QY    24 KOELLAHRFCCELLPQEQRTESSSLRAQVPFEQLISLPFLKANPEKERICRVFTSTSPAK 83
       :|||::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db     3 RDEIERLRKRFMKLD RDSSSGSIDKN-----EFMSIPGVSSNP LAGRIMEVFADADNSG 54
QY    84 DSLSEDFEFLDLLSVESD TATPDIKSHYAERIFXXXXXXXSRLLVNC LTGEGETR 143
       |:||:|||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db     55 D-VDPGEFITGLSIFSGRSKDKLRF AFKIYIDDKDGFI SNGELLEIVLKIMVG---SN 109
QY    144 LSASEMKQLIDNILESDIDRGITINLSEFOHVI 177
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Db     110 LDDELQLOQIYDRTRIVENSDGDGRLSFE EFKNAI 143


RESULT 6
US-08-720-625-4
; Sequence 4, Application US/08720625
; Patent No. 6242587
; GENERAL INFORMATION:
; APPLICANT: Naik, Vilas P.
; APPLICANT: Parise, Leslie V.
; TITLE OF INVENTION: CALCIUM-INTEGRIN BINDING PROTEIN
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bell, Seltzer, Park & Gibson
; STREET: P.O. Drawer 34009
; CITY: Charlotte
; STATE: NC 6242587th Carolina
; COUNTRY: USA
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/720,625
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sidley, Kenneth D.
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 5470-138
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-420-2200
; TELEFAX: 919-881-3175
; INFORMATION FOR SEQ ID NO: 4:
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Db 71 DHEFIVGTSQSVKGEDEQKLRFAFRIDYMDNDGFIISNGELFQVLKMMVG-----NNLKD 126

QY 147 SEMKOLIDNILESDIDRDGTINLSEFOHVI 177

Db 127 WOLQQLVDKSILVLDKGDGRISFEEFSADV 157

RESULT 9

US-08-655-352-8

; Sequence 8, Application US/08655352

; Patent No. 6077991

; GENERAL INFORMATION:

; APPLICANT: Bachettira W. Poovaiiah, Zhuhua Liu,

; APPLICANT: Shameekumar Patil, Dalsuke Takezawa

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR

; TITLE OF INVENTION: PRODUCTION OF MALE-STERILE PLANTS

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Kiarquist Sparkman Campbell Leigh &

; ADDRESSEE: Whinston, LLP

; STREET: One World Trade Center

; STREET: 121 S.W. Salmon Street

; STREET: Suite 1600

; CITY: Portland

; STATE: Oregon

; COUNTRY: United States of America

; ZIP: 97204

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Disk, 3-1/2 inch

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: MS DOS

; SOFTWARE: WordPerfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/655,352

; FILING DATE:

; CLASSIFICATION: 800

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/323,449

; FILING DATE: October 14, 1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Dow, Alan. E.

; REGISTRATION NUMBER: 35,123

; REFERENCE/DOCKET NUMBER: 4630-45000

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (503) 226-7391

; TELEFAX: (503) 228-9446

; INFORMATION FOR SEQ ID NO: 8:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 186 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; DESCRIPTION: Region of Drosophila frequen

; DESCRIPTION: (Gen2:Drofreg) with homology to 111y

; DESCRIPTION: CCAMK

US-08-655-352-8

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Best Local Similarity 22.3%; Pred. No. 1.4e-07;

Matches 44; Conservative 36; Mismatches 95; Indels 22; Gaps 5;

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Db 1 MGKSSSKLKQDTIDRLTDTYTFTEKEIRQWHKGLKDCPNGLLLEQGFIKIKQF----- 55

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Db 56 FPQGDPSKFAVLFRVFDEN-NDGSIFFEEFIRALSVTSKGL--DEKLQWAFRLYDVND 112

QY 121 XXXXXXXXSLVNL-----TGEGEDTRLASSEMQLIDNILESDIDRDGTINLSE 172

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QY 173 FOHVISRSPDFASSFKI 189

Db 167 FREGSKADPRIVQALSL 183

RESULT 10

US-09-258-016-8

; Sequence 8, Application US/09258016

; Patent No. 6362395

; GENERAL INFORMATION:

; APPLICANT: Bachettira W. Poovaiiah, Zhuhua Liu,

; APPLICANT: Shameekumar Patil, Dalsuke Takezawa

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR

; TITLE OF INVENTION: PRODUCTION OF MALE-STERILE PLANTS

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Kiarquist Sparkman Campbell Leigh &

; ADDRESSEE: Whinston, LLP

; STREET: One World Trade Center

; STREET: 121 S.W. Salmon Street

; STREET: Suite 1600

; CITY: Portland

; STATE: Oregon

; COUNTRY: United States of America

; ZIP: 97204

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Disk, 3-1/2 inch

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: MS DOS

; SOFTWARE: WordPerfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/258,016

; FILING DATE:

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Stephens Jr., Donald L.

; REGISTRATION NUMBER: 34,022

; REFERENCE/DOCKET NUMBER: 4630-51994

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (503) 226-7391

; TELEFAX: (503) 228-9446

; INFORMATION FOR SEQ ID NO: 8:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 186 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; DESCRIPTION: Region of Drosophila frequen

; DESCRIPTION: (Gen2:Drofreg) with homology to 111y

; DESCRIPTION: CCAMK

US-09-258-016-8

Query Match 13.9%; Score 126; DB 4; Length 186;

Best Local Similarity 22.3%; Pred. No. 1.4e-07;

Matches 44; Conservative 36; Mismatches 95; Indels 22; Gaps 5;

QY 1 MGGSGSRSLKELLAEYQDLTFLTKOELLAHRRFCCLLPQORTVESSLRAQVPFEQILS 60

Db 1 MGKSSSKLKQDTIDRLTDTYTFTEKEIRQWHKGLKDCPNGLLLEQGFIKIKQF----- 55

QY 61 LPELKANPFEKRICRVFSTSPAKDSLSFEDFLDLVSFSDTATPDIKSHYAFRIFFXXXXX 120

Db 56 FPQGDPSKFAVLFRVFDEN-NDGSIFFEEFIRALSVTSKGL--DEKLQWAFRLYDVND 112

QY 121 XXXXXXXXSLVNL-----TGEGEDTRLASSEMQLIDNILESDIDRDGTINLSE 172

Db 113 GYTREEMYNIVDAIYQWVGQPOSEDENT-----PQKRVDKIFDQMDKNHDKLTLLE 166

QY 173 FOHVISRSPDFASSFKI 189

Db 167 FREGSKADPRIVQALSL 183

Db 110 -----| | | : | | | : : |
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Qy 155 NILESDIDRDGTINLSEF-----QHVISRSPDFASSF 187
| : | | : | | : : | | |
Db 151 KIFRQMDINNDGKLSLEEFIKGAKSDPSIVRLLQCDPSSASQF 193

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Job time : 14 secs

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OM protein - protein search, using sw model

Run on: January 17, 2003, 12:45:39 ; Search time 11 Seconds
(without alignments)
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Perfect score: 904
Sequence: 1 MGGSGSRLSKELLAELYDILT.....EFQHVISRSPDFASSFKIVL 191

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Gapop 10.0 , Gapext 0.5

Searched: 120991 seqs, 19878514 residues

Total number of hits satisfying chosen parameters: 120991

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA:*

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- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
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- 6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
- 10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
- 12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
- 13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
- 14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	879	97.2	191	10	US-09-878-454A-2 Sequence 2, Appl1
2	867	95.9	191	12	US-10-109-885-2 Sequence 2, Appl1
3	309	34.2	187	10	US-09-802-116-2 Sequence 2, Appl1
4	146.5	16.2	170	12	US-10-109-885-3 Sequence 3, Appl1
5	136.5	15.1	195	10	US-09-999-602-3 Sequence 3, Appl1
6	132.5	14.7	195	10	US-09-999-602-4 Sequence 4, Appl1
7	130	14.4	214	10	US-09-999-602-1 Sequence 1, Appl1
8	106	11.7	220	10	US-09-350-874-26 Sequence 26, Appl1
9	101	11.2	220	10	US-09-350-874-24 Sequence 24, Appl1
10	101	11.2	252	10	US-09-350-874-20 Sequence 20, Appl1
11	101	11.2	270	10	US-09-350-874-14 Sequence 14, Appl1
12	98	10.8	270	10	US-09-350-874-18 Sequence 18, Appl1
13	96	10.6	225	10	US-09-350-874-30 Sequence 30, Appl1
14	96	10.6	252	10	US-09-350-874-22 Sequence 22, Appl1
15	96	10.6	252	10	US-09-350-874-28 Sequence 28, Appl1
16	96	10.6	252	10	US-09-350-874-42 Sequence 42, Appl1
17	96	10.6	257	10	US-09-350-874-16 Sequence 16, Appl1
18	90	10.0	216	10	US-09-350-874-6 Sequence 6, Appl1
19	90	10.0	227	10	US-09-350-874-8 Sequence 8, Appl1

20	90	10.0	227	10	US-09-350-874-10	Sequence 10, Appl1
21	90	10.0	245	10	US-09-350-874-4	Sequence 4, Appl1
22	89	9.8	216	9	US-09-965-528-15	Sequence 15, Appl1
23	89	9.8	216	10	US-09-350-874-2	Sequence 2, Appl1
24	85.5	9.5	142	10	US-09-910-071-4	Sequence 4, Appl1
25	85	9.4	642	9	US-09-554-000-6	Sequence 6, Appl1
26	85	9.4	656	9	US-09-554-000-8	Sequence 8, Appl1
27	84	9.3	642	9	US-09-554-000-2	Sequence 2, Appl1
28	84	9.3	652	9	US-09-554-000-4	Sequence 4, Appl1
29	82	9.1	229	10	US-09-350-874-70	Sequence 70, Appl1
30	82	9.1	233	10	US-09-350-874-49	Sequence 49, Appl1
31	82	9.1	250	10	US-09-350-874-72	Sequence 72, Appl1
32	80.5	8.9	172	12	US-10-109-885-4	Sequence 4, Appl1
33	79.5	8.8	139	10	US-09-864-761-34808	Sequence 34808, A
34	74	8.2	256	10	US-09-350-874-36	Sequence 36, Appl1
35	72.5	8.0	159	10	US-09-910-071-5	Sequence 5, Appl1
36	71.5	7.9	1210	9	US-10-025-380-692	Sequence 692, App
37	71.5	7.9	1210	10	US-09-922-217-692	Sequence 692, App
38	71.5	7.9	1210	10	US-09-833-263-692	Sequence 692, App
39	71.5	7.9	1548	9	US-10-025-380-1095	Sequence 1095, Ap
40	71.5	7.9	1548	10	US-09-922-217-1095	Sequence 1095, Ap
41	71	7.9	203	10	US-09-350-874-12	Sequence 12, Appl
42	71	7.9	256	10	US-09-350-874-32	Sequence 32, Appl
43	70.5	7.8	90	10	US-09-826-589-3	Sequence 3, Appl1
44	70.5	7.8	90	10	US-09-826-589-4	Sequence 4, Appl1
45	70.5	7.8	90	10	US-09-872-185B-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1
US-09-878-454A-2
Sequence 2, Application US/09878454A
Patent No. US20020064828A1
GENERAL INFORMATION:
APPLICANT: Montelro, et al.
TITLE OF INVENTION: Method of Controlling the Binding of Calmyrin to Present11
FILE REFERENCE: 4115-161
CURRENT APPLICATION NUMBER: US/09/878,454A
PRIOR FILING DATE: 2001-06-11
PRIOR APPLICATION NUMBER: 60/210,939
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 191
TYPE: PRT
ORGANISM: Homo sapiens
US-09-878-454A-2

Query Match 97.2%; Score 879; DB 10; Length 191;
Best Local Similarity 93.2%; Pred. No. 2e-92;
Matches 178; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 1 MGGSGSRLSKELLAELYDILFLTKQEIILAHRRFCCLPQORTVSSSLRAQVPFQILS 60
Db 1 MGGSGSRLSKELLAELYDILFLTKQEIILAHRRFCCLPQORTVSSSLRAQVPFQILS 60
QY 61 LPELKANPEKERICRVFSTPAKDSLSFEDFLDLSVFSDDTATPDIKSHYAFRTXXXXX 120
Db 61 LPELKANPEKERICRVFSTPAKDSLSFEDFLDLSVFSDDTATPDIKSHYAFRTXXXXX 120
QY 121 XXXXXXXXSRVNLCTGEGEDTRLASSEMQLIDNILEESDIDRDGTINSEFQHVISR 180
Db 121 GTLNREDLSRLVNLCTGEGEDTRLASSEMQLIDNILEESDIDRDGTINSEFQHVISR 180
QY 181 PDFASSFKIVL 191
Db 181 PDFASSFKIVL 191

RESULT 2

```
US-10-109-885-2
; Sequence 2; Application US/10109885
; Patent No. US20020119129A1
; GENERAL INFORMATION:
; APPLICANT: REVEL, Michel
; APPLICANT: CHEBATH, Judith
; APPLICANT: ABRAMOVITCH, Carolina
; TITLE OF INVENTION: NOVEL IFN RECEPTOR I BINDING PROTEIN, DNA ENCODING THEM, AND METH
; TITLE OF INVENTION: MODULATING CELLULAR RESPONSE TO INTERFERON
; FILE REFERENCE: REVEL-14A
; CURRENT FILING DATE: 2002-04-01
; PRIOR FILING DATE: 1999-10-18
; PRIOR FILING DATE: 1999-10-18
; PRIOR FILING DATE: 1998-01-15
; PRIOR FILING DATE: 1997-01-15
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 191
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-109-885-2
Query Match 95.9%; Score 867; DB 12; Length 191;
Best Local Similarity 92.1%; Pred. No. 4.7e-91;
Matches 176; Conservative 1; Mismatches 14; Indels 0; Gaps 0;
QY 1 MGGSGRSLSKELLAEQDLTFLTKQELLAHRRFCELLPQEQRTVLESSLRAQVPFEQILS 60
Db 1 MGGSGRSLSKELLAEQDLTFLTKQELLAHRRFCELLPQEQRSVLESSLRAQVPFEQILS 60
QY 61 LPKLANPFRKICRVFSTSPAKDSLSFEDFLDLSVFSATPDPIKSHYAFRIFXXXXX 120
Db 61 LPKLANPFRKICRVFSTSPAKDSLSFEDFLDLSVFSATPDPIKSHYAFRIFDXXX 120
QY 121 XXXXXXXXSRVNLCTGEGEDTRLSASEMKQLIDNILEESDIDRDGTINLSEFQHVISRS 180
Db 121 GTLNREDLSRVNLCTGEGEDTRLSASEMKQLIDNILEESDIDRDGTINLSEFQHVISRS 180
QY 181 PDFASFEKIVL 191
Db 181 PDFASFEKIVL 191
RESULT 3
US-09-802-116-2
; Sequence 2, Application US/09802116
; Patent No. US20020082406A1
; GENERAL INFORMATION:
; APPLICANT: Mathur, Brian
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. US20020082406A1el Human Kinase Interacting Protein and Polynu
; TITLE OF INVENTION: the Same
; FILE REFERENCE: LEX-0146-USA
; CURRENT FILING DATE: 2001-03-08
; PRIOR FILING DATE: 2000-03-08
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 187
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-802-116-2
Query Match 34.2%; Score 309; DB 10; Length 187;
Best Local Similarity 37.8%; Pred. No. 1e-27;
Matches 73; Conservative 39; Mismatches 69; Indels 12; Gaps 5;
US-10-109-885-3
; Sequence 3, Application US/10109885
; Patent No. US20020119129A1
; GENERAL INFORMATION:
; APPLICANT: REVEL, Michel
; APPLICANT: CHEBATH, Judith
; APPLICANT: ABRAMOVITCH, Carolina
; TITLE OF INVENTION: NOVEL IFN RECEPTOR I BINDING PROTEIN, DNA ENCODING THEM, AND
; TITLE OF INVENTION: MODULATING CELLULAR RESPONSE TO INTERFERON
; FILE REFERENCE: REVEL-14A
; CURRENT FILING DATE: 2002-04-01
; PRIOR FILING DATE: 1999-10-18
; PRIOR FILING DATE: 1999-10-18
; PRIOR FILING DATE: 1998-01-15
; PRIOR FILING DATE: 1997-01-15
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-10-109-885-3
Query Match 16.2%; Score 146.5; DB 12; Length 170;
Best Local Similarity 27.0%; Pred. No. 2.5e-09;
Matches 33; Conservative 29; Mismatches 55; Indels 5; Gaps 2;
QY 56 EQILSLPELKANPFRKICRVFSTSPAKDSLSFEDFLDLSVFSATPDPIKSHYAFRIF 115
Db 41 EEFMSLPELQNNPLVQRVIDIFDTD-GNGEVDKFEFEGVSQFSVKGDKQKLRFAFRY 99
QY 116 XXXXXXXXSRVNLCTGEGEDTRLSASEMKQLIDNILEESDIDRDGTINLSEFQHV 175
Db 100 DMDKDGYSISNGELFQVLKMMVG----NNLKDQLQIVDKTIINADKDGGRISFEFCA 155
QY 176 VI 177
Db 156 VV 157
RESULT 5
US-09-999-602-3
; Sequence 3, Application US/09999602
; Patent No. US20020091084A1
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti G.
; APPLICANT: Corley, Neil C.
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: HUMAN CALCIUM BINDING PROTEIN
; FILE REFERENCE: PF-0468-2 CON
```


SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 14
 LENGTH: 270
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-350-874-14

Query Match 11.2%; Score 101; DB 10; Length 270;
 Best Local Similarity 21.4%; Pred. No. 0.0007;
 Matches 42; Conservative 40; Mismatches 76; Indels 38; Gaps 7;

QY 11 ELLAEYQDLTFLTKQELLAHRRFCCELLPOEQRTVESSLRAQVPFEQILS--LPPELKAMP 68
 DB 91 EGLEQLOEQTKFTRELOVLYRGFKNECP-----SGIVNEENFKQIYSQFFPQGDSSN 143
 QY 69 FKERICRVFSTSPAKDSLSFEDFLDLVSFSDTATPDIKSHYAFRIFFXXXXXXX 128
 DB 144 YATFLFNADTN-HDGSVSFEDFVAGLSVIL-RGTVDRLNMAFNLYDLNKD----- 193
 QY 129 SRLVNCLTGE-----GEDT--RLSASEMKQILIDNILESDIDRDGTINLSEF 173
 DB 194 ---GCITKEEMLDIMKSIYDMGKYTPALRREAPREHVESFFOKMDRNKDGVTIEEF 249
 QY 174 OHVISRSPDFASSFKI 189
 DB 250 IESCQKXENIMRSMQL 265

RESULT 12
 US-09-350-874-18
 Sequence 18, Application US/09350874
 Patent No. US20020019020A1

GENERAL INFORMATION:
 APPLICANT: Rhodes, Kenneth
 APPLICANT: An, Wengqian
 TITLE OF INVENTION: METHODS FOR TREATING CARDIOVASCULAR DISORDERS
 FILE REFERENCE: MNI-069
 CURRENT APPLICATION NUMBER: US/09/350,874
 EARLIER APPLICATION NUMBER: USSN 60/110,277
 EARLIER FILING DATE: 1998-11-30
 EARLIER APPLICATION NUMBER: USSN 60/110,033
 EARLIER FILING DATE: 1998-11-25
 EARLIER APPLICATION NUMBER: USSN 60/109,333
 EARLIER FILING DATE: 1998-11-20
 EARLIER APPLICATION NUMBER: USSN 09/298,731
 NUMBER OF SEQ ID NOS: 72
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 18
 LENGTH: 270
 TYPE: PRT
 ORGANISM: Mus musculus
 US-09-350-874-18

Query Match 10.8%; Score 98; DB 10; Length 270;
 Best Local Similarity 22.8%; Pred. No. 0.0015;
 Matches 41; Conservative 36; Mismatches 65; Indels 38; Gaps 7;

QY 11 ELLAEYQDLTFLTKQELLAHRRFCCELLPOEQRTVESSLRAQVPFEQILS--LPPELKAMP 68
 DB 91 EGLEQLOEQTKFTRELOVLYRGFKNECP-----SGIVNEENFKQIYSQFFPQGDSSN 143
 QY 69 FKERICRVFSTSPAKDSLSFEDFLDLVSFSDTATPDIKSHYAFRIFFXXXXXXX 128
 DB 144 YATFLFNADTN-HDGSVSFEDFVAGLSVIL-RGTVDRLNMAFNLYDLNKD----- 193
 QY 129 SRLVNCLTGE-----GEDT--RLSASEMKQILIDNILESDIDRDGTINLSEF 173
 DB 194 ---GCITKEEMLDIMKSIYDMGKYTPALRREAPREHVESFFOKMDRNKDGVTIEEF 249

RESULT 13

US-09-350-874-30
 Sequence 30, Application US/09350874
 Patent No. US20020019020A1
 GENERAL INFORMATION:
 APPLICANT: Rhodes, Kenneth
 APPLICANT: An, Wengqian
 TITLE OF INVENTION: METHODS FOR TREATING CARDIOVASCULAR DISORDERS
 FILE REFERENCE: MNI-069
 CURRENT APPLICATION NUMBER: US/09/350,874
 EARLIER APPLICATION NUMBER: USSN 60/110,277
 EARLIER FILING DATE: 1998-11-30
 EARLIER APPLICATION NUMBER: USSN 60/110,033
 EARLIER FILING DATE: 1998-11-25
 EARLIER APPLICATION NUMBER: USSN 60/109,333
 EARLIER FILING DATE: 1998-11-20
 EARLIER APPLICATION NUMBER: USSN 09/298,731
 NUMBER OF SEQ ID NOS: 72
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 30
 LENGTH: 225
 TYPE: PRT
 ORGANISM: Rattus sp.
 US-09-350-874-30

Query Match 10.6%; Score 96; DB 10; Length 225;
 Best Local Similarity 22.8%; Pred. No. 0.002;
 Matches 41; Conservative 35; Mismatches 66; Indels 38; Gaps 7;

QY 11 ELLAEYQDLTFLTKQELLAHRRFCCELLPOEQRTVESSLRAQVPFEQILS--LPPELKAMP 68
 DB 46 EGLEQLOEQTKFTRELOVLYRGFKNECP-----SGIVNEENFKQIYSQFFPQGDSSN 98
 QY 69 FKERICRVFSTSPAKDSLSFEDFLDLVSFSDTATPDIKSHYAFRIFFXXXXXXX 128
 DB 99 YATFLFNADTN-HDGSVSFEDFVAGLSVIL-RGTVDRLNMAFNLYDLNKD----- 148
 QY 129 SRLVNCLTGE-----GEDT--RLSASEMKQILIDNILESDIDRDGTINLSEF 173
 DB 149 ---GCITKEEMLDIMKSIYDMGKYTPALRREAPREHVESFFOKMDRNKDGVTIEEF 204

RESULT 14
 US-09-350-874-22
 Sequence 22, Application US/09350874
 Patent No. US20020019020A1

GENERAL INFORMATION:
 APPLICANT: Rhodes, Kenneth
 APPLICANT: An, Wengqian
 TITLE OF INVENTION: METHODS FOR TREATING CARDIOVASCULAR DISORDERS
 FILE REFERENCE: MNI-069
 CURRENT APPLICATION NUMBER: US/09/350,874
 EARLIER APPLICATION NUMBER: USSN 60/110,277
 EARLIER FILING DATE: 1998-11-30
 EARLIER APPLICATION NUMBER: USSN 60/110,033
 EARLIER FILING DATE: 1998-11-25
 EARLIER APPLICATION NUMBER: USSN 60/109,333
 EARLIER FILING DATE: 1998-11-20
 EARLIER APPLICATION NUMBER: USSN 09/298,731
 NUMBER OF SEQ ID NOS: 72
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 22
 LENGTH: 252
 TYPE: PRT
 ORGANISM: Rattus sp.
 US-09-350-874-22

Query Match 10.6%; Score 96; DB 10; Length 252;
 Best Local Similarity 22.8%; Pred. No. 0.0024;
 Matches 41; Conservative 35; Mismatches 66; Indels 38; Gaps 7;

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QY 11 ELLAEYQDUFTLTQOEILLAHRRFCELLPQEQTVESSLRAQVPFEQILS--LPELKANP 68
| | : : | | : : : | | | : : | : | | | : : :
Db 73 EGLEQLQEQTKFTRRELQVLYRGFKNECP-----SGIVNEENFKQIYSQFFPQGDSSN 125

QY 69 FKERICRVFSTSPAKDSLSFEDFLDLLSVFSDTATPDIKSHYAFRIFXXXXXXXXXXXXXX 128
: | | : | : | : | : | : | : | : | : | : | : | :
Db 126 YATFLFNADFDTN-HDGSVSFEDFVAGLSVIL-RGTIDRLSWAFNLYDLNKD----- 175

QY 129 SRLVNCUTGE-----GEDT--RLSASEMKQLIDNILEESDIDRDCGTINLSEF 173
| | | | | | | | | | | | | | : : : | : | : | : |
Db 176 ----GCITKEEMLDIMKSIYDMGKYTYPALREEAPREHVESFFQKMDRKNKDGVVITIEEF 231

```


GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 17, 2003, 12:44:38 ; Search time 17 Seconds

(without alignments)
1080.099 Million cell updates/sec

Title: US-09-878-454A-2X

Perfect score: 904

Sequence: 1 MGGSGSRLSKELLAERYDIT.....EFQHVISRSPDFASSFKIVL 191

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 segs, 96134422 residues
Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	Query Match	Length	DB	ID	Description
1	367	40.6	311	2	T21563	hypothetical prote
2	171.5	19.0	174	2	T41632	probable calcineur
3	164.5	18.2	175	2	JH0462	phosphoprotein pho
4	160.5	17.8	174	2	T47245	calcineurin regula
5	146.5	16.2	170	1	A33391	calcineurin regula
6	146.5	16.2	170	1	S34127	calcineurin regula
7	146.5	16.2	170	1	JC1220	calcineurin regula
8	146.5	16.2	216	1	S42716	calcineurin regula
9	144.5	16.0	369	2	T22708	hypothetical prote
10	140.5	15.5	195	2	T28047	hypothetical prote
11	139.5	15.4	213	2	T31775	hypothetical prote
12	136.5	15.1	170	2	JC5174	calcineurin regula
13	135.5	15.0	170	2	JC7242	calcineurin regula
14	132.5	14.7	170	2	A44307	calcineurin regula
15	130.5	14.4	179	2	JC1221	calcineurin regula
16	130.5	14.4	226	2	T51357	calcineurin regula
17	128.5	14.2	165	2	PS0261	calcineurin regula
18	128.5	14.2	176	2	JQ1232	calcineurin regula
19	123.5	13.7	190	2	T20725	hypothetical prote
20	121	13.4	192	2	T01375	calcium sensor hom
21	118.5	13.1	226	2	T08923	calcineurin B-like
22	117	12.9	191	2	JH0815	neural visinin-lik
23	117	12.9	193	2	JH0816	neural visinin-lik
24	117	12.9	246	2	T05308	hypothetical prote
25	117	12.9	246	2	H85387	hypothetical prote
26	116	12.8	193	2	I50676	gene Rem-1 protein
27	116	12.8	193	2	S47565	calcium-binding pr
28	114.5	12.7	213	2	T51356	calcineurin B-like
29	114	12.6	190	2	I51686	frequentin - Africa

30	111	12.3	224	2	F96668	protein FIN19.5 (1
31	108	11.9	191	2	JH0605	neural visinin-lik
32	108	11.9	191	2	A48979	visinin-like prote
33	106	11.7	190	2	A55666	neurocalcin - fru1
34	102	11.3	193	2	JH0616	neurocalcin (clone
35	101	11.2	270	2	JC7631	K+ channel-interac
36	99	11.0	190	2	S61168	hypothetical prote
37	98.5	10.9	172	2	S38531	caltractin - mouse
38	97	10.7	165	2	A44103	neurocalcin beta -
39	97	10.7	193	2	JC2186	hippocalcin - huma
40	96.5	10.7	155	2	S38877	troponin C isoform
41	96	10.6	151	2	A71409	calmodulin 8 (lipo
42	96	10.6	190	2	S58303	related to neuroa
43	95.5	10.6	172	2	I38424	centrin - human
44	94.5	10.5	158	2	A38397	troponin C-1 - gla
45	94.5	10.5	571	2	T00835	calcium-dependent

ALIGNMENTS

RESULT 1
T21563
hypothetical protein F30A10.1 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C/Accession: T21563
R/Barlow, K.
submitted to the EMBL Data Library, October 1996
A/Reference number: Z19442
A/Accession: T21563
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-311 <FWL>
A/Cross-references: EMBL:Z81072; PIDN:CAH03019.1; GSPDB:GN00019; CESP:F30A10.1
A/Experimental source: clone F30A10
C/Genetics:
A/Gene: CESP:F30A10.1
A/Map position: 1
A/Introns: 106/2; 139/3; 190/3; 240/1

Query Match 40.6%; Score 367; DB 2; Length 311;
Best Local Similarity 39.6%; Pred. No. 4.9e-26;
Matches 82; Conservative 39; Mismatches 60; Indels 26; Gaps 5;

QY 1 MGGSGSRLS-----KELLAERYDITFLTKQELLAAHRCCELLPQEQRTVESS 48
DB 111 MGNMSSLSSELNLFSGVFTREQDDEYQDCTFTRKDIIRLYKRYALPNHK--VPTN 167
QY 49 LRAQVP-----FEQILSLPELKANPFKERICRVFSTSPAKDSLSFEDFLDLSVFSDTA 102
DB 168 MGNMRAITTLTFEEVERKMPKELKNPFKRICEVFS-EDGRNLSFDLDMFSVFSSEMA 226
QY 103 TPDIKSHYAFRIFFXXXXXXXSRVNLCTGEGEDFRLSASEMKOLIDNILESDI 162
DB 227 PLQIKLYAFRIYDYDDELIGHDDLKMRSLTRD---ELSDVEVEFIIRIIEADL 282
QY 163 DRDGTINLSEFOHVISRSPDFASSFKI 189
DB 283 DGDSSINFAEFEEHVSRSPDFIRTFHI 309

RESULT 2
T41632
probable calcineurin b subunit - fission yeast (Schizosaccharomyces pombe)
C/Species: Schizosaccharomyces pombe
C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 04-Feb-2000
C/Accession: T41632
R/McDougall, R.M.; Rajandream, M.A.; Barfell, B.G.; Ramsperger, U.; Pohl, T.
submitted to the EMBL Data Library, August 1999
A/Reference number: Z22005
A/Accession: T41632
A/Status: preliminary; translated from GB/EMBL/DBJ

Db 1 MGNSSSLMLRDEEIEIMSETEFNNOIVRLYSRFLSLDKKGGLSR-----DDFL 52
 QY 60 SLPELKANPEKERICRVSTSPA-----KDSISEFEDLDLSVFSPTATPDIKSH---- 109
 Db 53 NPELAVNPLCDRIVDAFTLASSNGDNEQOLNRFQVRILAHFQPISR--VKKNALNS 110
 QY 110 -----YAFRIEYXXXXXXXSRVLVNCITGEGEDTRLSASEMKQIDNILEESDID 163
 Db 111 RKDKLFAFKMYDLNKNNDYITREEFKVILNSMVG---ANTSDQLDKIADRTIEADAD 166
 QY 164 RDGTINLSEFOHVISRS 180
 Db 167 RDGKISFDEFCRAMEXT 183

RESULT 11
 T31775
 hypothetical protein F59D6.7 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
 C:Accession: T31775
 R:Bradshaw, H.; Graves, T.
 submitted to the EMBL Data Library, July 1997
 A:Description: The sequence of C. elegans cosmid F59D6.
 A:Reference number: 221083
 A:Accession: T31775
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-213 <BRA>
 A:Cross-references: EMBL:AF016435; PIDN:AAB65882.1; GSPDB:GN00023; CESP:F59D6.7
 A:Experimental source: strain Bristol N2; clone F59D6
 C:Genetics:
 A:Gene: CESP:F59D6.7
 A:Map position: 5
 A:Introns: 24/2; 60/1; 135/1

Query Match 15.4%; Score 139.5; DB 2; Length 213;
 Best Local Similarity 22.1%; Pred. No. 1.8e-05;
 Matches 47; Conservative 40; Mismatches 81; Indels 45; Gaps 7;
 QY 1 MGSGLSRL-----SKELLAEXQ-----DLTFLTKQEILLAHRRFCCELLPOE 41
 Db 1 MGNSSSLMLRDEEIEIMSETEFNNOIVRLYSRFLSLDKKGGLSR-----DDFL 52
 QY 42 QRTVSSSLRAQVPFEQILSLPELKANPEKERICRVSTSPA-----SLSFEDLDL 95
 Db 57 ----DKNGQYLSRDDFLNVELAVNPLGDRITIDAFITLGDSDGDSKSGQLTFROFVRIL 112
 QY 96 SVF-----SDTATPDIKS--HYAFRIEYXXXXXXXSRVLVNCITGEGEDTRLSAS 147
 Db 113 AHQPIISKVKDNALNSRKDKLFAFKMYDLNKNNDYITREEFKVILNSMVG---ANTSD 166
 QY 148 EMQOLIDNILEESDIDRDGTINLSEFOHVISRS 180
 Db 169 QLDKIADKTLEADQDRDGKISFDEFCRAMEXT 201

RESULT 12
 JC5174
 calcineurin regulatory chain 2 - fruit fly (Drosophila melanogaster)
 N:Alternate names: calcineurin beta subunit; calcineurin chain B-2; phosphoprotein phos
 C:Species: Drosophila melanogaster
 C:Date: 16-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 13-Aug-1999
 C:Accession: JC5174
 R:Warren, W.D.; Phillips, A.M.; Howells, A.J.
 Gene 177, 149-153, 1996
 A>Title: Drosophila melanogaster contains both x-linked and autosomal homologues of the
 A:Reference number: JC5174; MUID:97080515; PMID:8921860
 A:Accession: JC5174
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-170 <WAR>
 A:Cross-references: GB:U56245; NID:g1336009; PIDN:AAC47350.1; PID:g1336010

C:Comment: This protein is the calcium binding chain of calcineurin, involved in
 C:Genetics:
 A:Gene: dcnb2
 C:Complex: heterodimer with calcineurin catalytic chain
 C:Superfamily: calmodulin; calmodulin repeat homology
 C:Keywords: blocked amino end; calcium binding; duplication; EF hand; heterodimer;
 F;2-170/Product: calcineurin regulatory chain #status predicted <MAT>
 F;18-49/Domain: calmodulin repeat homology <EF1>
 F;50-82/Domain: calmodulin repeat homology <EF2>
 F;87-119/Domain: calmodulin repeat homology <EF3>
 F;128-160/Domain: calmodulin repeat homology <EF4>
 F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
 F;3/Modified site: aspartic acid (Asn) #status predicted

Query Match 15.1%; Score 136.5; DB 2; Length 170;
 Best Local Similarity 21.9%; Pred. No. 2.6e-05;
 Matches 39; Conservative 39; Mismatches 81; Indels 19; Gaps 4;
 QY 3 GSGSRLSKELLAQYDITLTKQEILLAHRRFCCELLPOEQRTVSSSLRAQVPFEQILSLP 62
 Db 2 GNETSLPMEMCSNFD-----ADEIRRLGRF-----RKLDLNSGALSVDEFMSLP 47
 QY 63 ELKANPEKERICRVSTSPA KDSLSFEDLDLSVFSPTATPDIKSHYAFRIEYXXXXXX 122
 Db 48 ELQONPLVQRYVIDIFD-ADNGEVDKEFEIGVSQFSVKGDKLSKLRAFRITDMNDGY 106
 QY 123 XXXXXSRVLVNCITGEGEDTRLSASEMKQIDNILEESDIDRDGTINLSEFOHVISRS 180
 Db 107 ISNGELFQVLKMWG-----NNLKDTQLQIVDKITIGFADKDEGKISFDEFCVGN 160

RESULT 13
 JC7242
 calcineurin regulatory subunit, calcineurin B - scallop (Patinopecten yessoensis)
 N:Alternate names: Ca2+/calmodulin-dependent phosphoprotein phosphatase regulatory
 C:Species: Patinopecten yessoensis (Yesso scallop)
 C:Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 21-Jul-2000
 C:Accession: JC7242; PC7070
 R:Uryu, M.; Nakatomi, A.; Watanabe, M.; Hatsuse, R.; Yazawa, M.
 J. Biochem. 127, 739-746, 2000
 A>Title: Molecular cloning of cDNA encoding two subunits of calcineurin from scallop.
 A:Reference number: JC7241
 A:Accession: JC7242
 A:Molecule type: mRNA
 A:Residues: 1-170 <URY>
 A:Cross-references: DDBJ:AB041524
 A:Experimental source: testis
 A:Accession: PC7070
 A:Molecule type: protein
 A:Residues: 12-68;73-85;92-170 <UR2>
 C:Comment: This protein, one of Ca2+/calmodulin-dependent enzyme, is a testis-spec.
 to the regulation of flagellar motility.
 C:Genetics:
 A:Gene: cnb
 C:Superfamily: calmodulin; calmodulin repeat homology
 C:Keywords: calcium binding; EF hand; flagellar rotation; myristylation; phosphopr
 Query Match 15.0%; Score 135.5; DB 2; Length 170;
 Best Local Similarity 22.3%; Pred. No. 3.2e-05;
 Matches 39; Conservative 38; Mismatches 79; Indels 19; Gaps 4;
 QY 3 GSGSRLSKELLAQYDITLTKQEILLAHRRFCCELLPOEQRTVSSSLRAQVPFEQILSLP 62
 Db 2 GNETSLPMELCSNFD-----PDEIKRLGRF-----RKLDLNSGSLSVDEFMTLP 47
 QY 63 ELKANPEKERICRVSTSPA KDSLSFEDLDLSVFSPTATPDIKSHYAFRIEYXXXXXX 122
 Db 48 ELQONPLVQRYVIDIFD-DNGEVDKEFEIGVSQFSVKGDKLSKLRAFRITDMNDGY 106
 QY 123 XXXXXSRVLVNCITGEGEDTRLSASEMKQIDNILEESDIDRDGTINLSEFOHYI 177
 Db 107 ISNGELFQVLKMWG-----NNLKDTQLQIVDKITIHADADGDGKISFEFCAYV 157

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 17, 2003, 12:43:38 ; Search time 12 Seconds
(without alignments)
660.165 Million cell updates/sec

Title: US-09-878-454A-2X
Perfect score: 904
Sequence: 1 MGGSGSRSLSKELLAEXQDLT.....EFOHVISRSPDFASSFKIVL 191

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
1	879	97.2	191	1. KIP1_HUMAN	Q99828 homo sapien
2	831	91.9	191	1. KIP1_MOUSE	Q920f4 mus musculu
3	830	91.8	191	1. KIP1_RAT	Q9r010 rattus norv
4	302	33.4	187	1. KIP2_MOUSE	Q92309 mus musculu
5	299	33.1	187	1. KIP2_HUMAN	O75838 homo sapien
6	176.5	19.5	177	1. CALB_NAEGR	P42322 naegleria g
7	171.5	19.0	174	1. CALB_SCHPO	Q9u093 schizosacch
8	160.5	17.8	174	1. CALB_NEUCR	P87072 neurospora
9	159.5	17.6	174	1. CALB_YEAST	P25296 saccharomyc
10	146.5	16.2	169	1. CALB_HUMAN	P06705 homo sapien
11	146.5	16.2	169	1. CALB_MOUSE	Q63810 mus musculu
12	136.5	15.1	170	1. CA22_MOUSE	Q24214 drosophila
13	135	14.9	194	1. CA22_MOUSE	Q62877 mus musculu
14	132.5	14.7	170	1. CALB_DROME	P48451 drosophila
15	131	14.5	194	1. CA22_HUMAN	Q99653 homo sapien
16	130.5	14.4	178	1. CALC_MOUSE	Q63811 mus musculu
17	130	14.4	214	1. TESC_MOUSE	Q96bs2 homo sapien
18	128.5	14.2	175	1. CALC_RAT	P28470 rattus norv
19	128	14.2	214	1. TESC_MOUSE	Q9jkl5 mus musculu
20	123.5	13.7	189	1. NCS2_CABEL	P36609 caenorhabdi
21	121.5	13.4	186	1. FREQ_DROME	P37236 drosophila
22	112	12.4	190	1. VIS2_RAT	P35333 rattus norv
23	112	12.4	192	1. VIS3_MOUSE	P35333 mus musculu
24	111	12.3	192	1. VIS3_CHICK	P42324 gallus galli
25	111	12.3	192	1. VIS3_HUMAN	P37235 homo sapien
26	109	12.1	189	1. NCS1_HUMAN	P36610 homo sapien
27	109	12.1	189	1. NCS1_XENLA	Q91614 xenopus lae
28	108	11.9	190	1. APLC_APLCA	Q16981 aplysia cal
29	107.5	11.9	195	1. H520_HUMAN	O43745 homo sapien
30	103	11.4	190	1. VIS1_HUMAN	P28677 homo sapien
31	103	11.4	192	1. NCAD_MOUSE	Q91x97 mus musculu
32	101	11.2	189	1. NCAD_DROME	P42325 drosophila
33	101	11.2	190	1. NCS1_CABEL	P36608 caenorhabdi

34	100	11.1	192	1	NCAD_CHICK	O12953 gallus galli
35	98.5	10.9	172	1	CATR_MOUSE	P41209 mus musculu
36	97	10.7	165	1	NCAB_BOVIN	P29104 bos taurus
37	97	10.7	192	1	NCAD_HUMAN	P29554 homo sapien
38	96.5	10.7	155	1	TPC2_DROME	P47948 drosophila
39	95.5	10.6	172	1	CAT2_HUMAN	O12798 homo sapien
40	94.5	10.5	158	1	TPC1_BALNU	P21797 balanus nub
41	94	10.4	189	1	NCS1_YEAST	Q06389 saccharomyc
42	94	10.4	192	1	HIPP_HUMAN	P32076 homo sapien
43	94	10.4	804	1	KDGB_HUMAN	O9y6t7 homo sapien
44	93	10.3	192	1	NECX_APLCA	Q16982 aplysia cal
45	92.5	10.2	155	1	TPC3_DROME	P47949 drosophila

ALIGNMENTS

RESULT 1
KIP1_HUMAN
ID KIP1_HUMAN STANDARD; PRT; 191 AA.
AC Q99828; 000735; 000693; Q99971; Q96J54;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Calcium and integrin-binding protein 1 (Calmyrin) (DNA-PKcs
DE Interacting protein) (Kinase interacting protein) (KIP) (CIB) (SNK
DE Interacting protein 2-28) (SIP2-28).
GN CIB1 OR PRKDCIP OR KIP OR CIB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Yuan O.;
RT "SNK, a Ser/Thr protein kinase, associated proteins.";
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA MEDLINE=98040126; PubMed=9372844;
RX Wu X., Lieber M.R.;
RT "Interaction between DNA-dependent protein kinase and a novel protein,
RT KIP.";
RL Mutat. Res. 385:13-20(1997).
RN [3]
RP SEQUENCE FROM N.A.
RX TISSUE=Fetal liver;
RC MEDLINE=97184102; PubMed=9030514;
RA Nalk U.P., Patel P.M., Parise L.V.;
RT "Identification of a novel calcium-binding protein that interacts
RT with the integrin alpha1b cytoplasmic domain.";
RL J. Biol. Chem. 272:4651-4654(1997).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=20284952; PubMed=10826701;
RA Hattori A., Seki N., Hayashi A., Kozuma S., Saito T.;
RT "Genomic structure of mouse and human genes for DNA-PKcs interacting
RT protein (KIP).";
RL DNA Seq. 10:415-418(2000).
RN [5]
RP SEQUENCE FROM N.A.
RX TISSUE=Cervix;
RA Strausberg R.;
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
RN [6]
RP STRUCTURE BY NMR OF 9-191.
RX MEDLINE=20283154; PubMed=10822252;
RA Hwang P.M., Vogel H.J.;
RT "Structures of the platelet calcium- and integrin-binding protein and
RT the alpha1b-integrin cytoplasmic domain suggest a mechanism for
RT calcium-regulated recognition; homology modelling and NMR studies.";
RL J. Mol. Recognit. 13:83-92(2000).
CC -1- FUNCTION: MAY CONVERT THE INACTIVE CONFORMATION OF INTEGRIN ALPHA-

DR SMART; SM00054; EFh; 2.
 DR PROSITE; PS00018; EF_HAND; 2.
 KW Calcium-binding; Repeat.
 FT CA_BIND 116 127 EF_HAND 1 (POTENTIAL).
 FT CA_BIND 161 172 EF_HAND 2 (POTENTIAL).
 SQ SEQUENCE 191 AA; 21763 MW; C85B603A19F9D9AC CRC64;

Query Match 91.8%; Score 831; DB 1; Length 191;
 Best Local Similarity 88.0%; Pred. No. 5.6e-72;
 Matches 168; Conservative 3; Mismatches 20; Indels 0; Gaps 0;

OY 1 MGGSGSRLSKELLAAYODLTFLTKQELLHAHRRFCCELLPQEQRTVESSLRAQVPFEQILS 60
 DB 1 MGGSGSRLSKELLAAYODLTFLTKQELLHAHRRFCCELLPQEQRTVESSLRAQVPFEQILS 60
 OY 61 LPELKANPEKERICRVFSTSPAKSLSFEDFLDLLSVFSPTATPDIKSHYAFRIFFXXXXX 120
 DB 61 LPELKANPEKERICRVFSTSPAKSLSFEDFLDLLSVFSPTATPDIKSHYAFRIFFDDDD 120
 OY 121 XXXXXXXXSRVLNCLTGEEDTRLSASEMKOLIDNILESDIDRDGTINLSEFOHVISRS 180
 DB 121 GTLDREDLSQVLNCLTGEEDTRLSASEMKOLIDNILESDIDRDGTINLSEFOHVISRS 180
 OY 181 PDFASSEFKIVL 191
 DB 181 PDFASSEFKIVL 191

RESULT 3

KIP1_RAT
 ID KIP1_RAT STANDARD; PRT; 191 AA.
 AC 09R010;

DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Calcium and integrin-binding protein 1 (Calmyrin) (DNA-PKcs
 DE interacting protein) (Kinase interacting protein) (KIP) (CIB).
 GN CIB1 OR PRKDCIP OR KIP OR CIB.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99452760; PubMed=10523297;
 RA Kaushelmann G., Weiler M., Wulff P., Jessberger S., Konietzko U.,
 RA Scafield J., Staubli U., Bereliter-Hahn J., Streibhardt K., Kuhl D.;
 RT "The polo-like protein kinases Fnk and Snk associate with a Ca(2+)-and
 RT integrin-binding protein and are regulated dynamically with synaptic
 RT plasticity.";
 RL EMO J. 18:5528-5539(1999).

-1- FUNCTION: MAY CONVERT THE INACTIVE CONFORMATION OF INTEGRIN ALPHA-
 IIB/BETA3 TO AN ACTIVE FORM THROUGH THE BINDING TO THE INTEGRIN
 CYTOPLASMIC DOMAIN (BY SIMILARITY).
 CC -1- SUBUNIT: INTERACTS WITH THE HETERODIMERIC INTEGRIN ALPHA-
 IIB/BETA3. INTERACTS WITH THE PROTEIN KINASES SNK AND WITH THE
 CC REGION IMMEDIATELY UPSTREAM OF THE KINASE DOMAIN OF DNA-PK (BY
 CC SIMILARITY).
 CC -1- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.

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DR EMBL; AF136585; AAF08368.1; -
 DR HSSP; Q99828; IDGV.
 DR InterPro; IPR002048; EF-hand.
 DR Pfam; PF00036; efhand; 2.
 DR ProDom; PD000012; EF-hand; 1.

DR SMART; SM00054; EFh; 2.
 DR PROSITE; PS00018; EF_HAND; 2.
 KW Calcium-binding; Repeat.
 FT CA_BIND 116 127 EF_HAND 1 (POTENTIAL).
 FT CA_BIND 161 172 EF_HAND 2 (POTENTIAL).
 SQ SEQUENCE 191 AA; 21800 MW; 3B00B0228879FC7 CRC64;

Query Match 91.8%; Score 830; DB 1; Length 191;
 Best Local Similarity 88.0%; Pred. No. 7e-72;
 Matches 168; Conservative 2; Mismatches 21; Indels 0; Gaps 0;

OY 1 MGGSGSRLSKELLAAYODLTFLTKQELLHAHRRFCCELLPQEQRTVESSLRAQVPFEQILS 60
 DB 1 MGGSGSRLSKELLAAYODLTFLTKQELLHAHRRFCCELLPQEQRTVESSLRAQVPFEQILS 60
 OY 61 LPELKANPEKERICRVFSTSPAKSLSFEDFLDLLSVFSPTATPDIKSHYAFRIFFXXXXX 120
 DB 61 LPELKANPEKERICRVFSTSPAKSLSFEDFLDLLSVFSPTATPDIKSHYAFRIFFDDDD 120
 OY 121 XXXXXXXXSRVLNCLTGEEDTRLSASEMKOLIDNILESDIDRDGTINLSEFOHVISRS 180
 DB 121 GTLDREDLSQVLNCLTGEEDTRLSASEMKOLIDNILESDIDRDGTINLSEFOHVISRS 180
 OY 181 PDFASSEFKIVL 191
 DB 181 PDFASSEFKIVL 191

RESULT 4

KIP2_MOUSE
 ID KIP2_MOUSE STANDARD; PRT; 187 AA.
 AC 09Z309;

DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Kinase interacting protein 2 (KIP 2).
 GN KIP2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain, and Testis;
 RX MEDLINE=99132027; PubMed=9931475;
 RA Seki N., Hattori A., Hayashi A., Kozuma S., Ohira M., Horii T.,
 RA Saito T.;
 RT "Structure, expression profile and chromosomal location of an isolog
 RT of DNA-PKcs interacting protein (KIP) gene.";
 RL Blochm. Biophys. Acta 1444:143-147(1999).

-1- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
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DR EMBL; AB016080; BAA36545.1; -
 DR HSSP; Q99828; IDGV.
 DR MGI; MGI:1929293; KIP2.
 DR InterPro; IPR002048; EF-hand.
 DR Pfam; PF00036; efhand; 3.
 DR ProDom; PD000012; EF-hand; 1.
 DR SMART; SM00054; EFh; 2.
 DR PROSITE; PS00018; EF_HAND; 2.
 KW Calcium-binding; Repeat.
 FT CA_BIND 116 127 EF_HAND 1 (POTENTIAL).
 FT CA_BIND 157 168 EF_HAND 2 (POTENTIAL).
 SQ SEQUENCE 187 AA; 21703 MW; D21D21DCBD0B6F5C CRC64;

Query Match 33.4%; Score 302; DB 1; Length 187;
Best Local Similarity 34.3%; Pred. No. 9.2e-22;
Matches 69; Conservative 43; Mismatches 61; Indels 28; Gaps 6;

QY 1 MGGSGRLSKELLAQYQDLTFLTKQEILLAHRRFCE---LLPQEQRTVSSSLRAQVPFE 56
DB 1 MGNKQTIETEEQLDNYQDCTFFNKKDILKLHARFELAPNLVPMYR---KSPIVHVPMS 57

QY 57 QILSLPELKANPKERICRVFSTSPAKDSLSFEDFLDLLSVFSDTATPDIKSHVAFRIFX 116
DB 58 LIQMPELRNPKERIVEAFS-EDGEGNLTNDFVDMFVSLCESAPRELKANVAFKIYD 116

QY 117 XXXXXXXXXXSRVNLCLTGEDED---TRLASSEMKG-----LIDNILEESDIDRDGTI 168
DB 117 FNTD-----NFICKEDLEMTLRLTKSELEDEVLVCDKVIEADLDGDKL 164

QY 169 NLSEFQHVISRSPDFASSFKI 189
DB 165 GFADFEDMIKAPDFLSTFHI 185

RESULT 5
KIP2_HUMAN
ID KIP2_HUMAN STANDARD; PRT; 187 AA.
AC O75838;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Kinase interacting protein 2 (KIP 2).
GN KIP2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Fetal brain;
RX MEDLINE=99132027; PubMed=9931475;
RA Seki N., Hattori A., Hayashi A., Kozuma S., Ohira M., Hori T.,
RA Saito T.;
RT "Structure, expression profile and chromosomal location of an isolog
RT of DNA-PKcs interacting protein (KIP) gene."
RL Biochim. Biophys. Acta 1444:143-147(1999).
CC -!- TISSUE SPECIFICITY: UBIQUITOUS.
CC -!- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AB012955; BAA33584.1; -
CC DR HSSP; Q99828; 1DGV.
CC DR MIM; 605564; -
CC DR InterPro; IPR002048; EF-hand.
CC DR Pfam; PF00036; ehand; 3.
CC DR ProDom; PD000012; EF-hand; 1.
CC DR SMART; SM00054; EFh; 2.
CC DR PROSITE; PS00018; EF_HAND; 2.
CC KW Calcium-binding; Repeat.
CC FT CA_BIND 116 127 EF-HAND 1 (POTENTIAL).
CC FT CA_BIND 157 168 EF-HAND 2 (POTENTIAL).
CC SQ SEQUENCE 187 AA; 21643 MW; D51F6C25AD381BEF CRC64;

Query Match 33.1%; Score 299; DB 1; Length 187;
Best Local Similarity 34.3%; Pred. No. 1.8e-21;
Matches 69; Conservative 42; Mismatches 62; Indels 28; Gaps 6;

QY 1 MGGSGRLSKELLAQYQDLTFLTKQEILLAHRRFCE---LLPQEQRTVSSSLRAQVPFE 56
DB 1 MGNKQTIETEEQLDNYQDCTFFNKKDILKLHARFELAPNLVPMYR---KSPIVHVPMS 57

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Db      1 MGNTISSLRPEEVEEMQKGTNFTQKEIKKLYKRFFKKLDDKGNGTISK-----DEFIM 52
OY      61 LPFLKANPFKERICRVFSTSPAKDSLSFEFDLLSVFSDTATPDIKSHYAFRIFXXXXX 120
        :||| || :|:| : |::|::| |||: |::|:
Db      53 IPELAVNPVLYKRVISIFDEN-GDGSVNEKEFIALSVFNAGDGQRKLLEFAFKVYDIDGD 111
OY      121 XXXXXXXXXSRLVNCLTGEGETRUSASEMKOLIDNILEESDIDRDGTINLSEFGHVIS 178
Db      112 GYISNGELFTVLKMVG-----NNLSDVQLQIVDKITILEADEDGDKISFEFEAKTL 165

RESULT 7
CALB_SCHPO
ID CALB_SCHPO STANDARD; PRT; 174 AA.
AC Q9U993;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Calcineurin B subunit (Protein phosphatase 2B regulatory subunit)
DE (Calcineurin regulatory subunit).
OS CNBI OR SPC830.06.
ON Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OX Schizosaccharomyces.
NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE-21848401; PubMed-11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Felwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., Mclean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Gymnopoulos B.,
RA Welltens I., Vanstreets E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gallardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerretti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RL "The genome sequence of Schizosaccharomyces pombe.";
CC Nature 415:871-880(2002).
CC -!- FUNCTION: REGULATORY SUBUNIT OF CALCINEURIN, A CALCIUM-DEPENDENT,
CC CALMODULIN STIMULATED PROTEIN PHOSPHATASE. CONFERS CALCIUM
CC SENSITIVITY (BY SIMILARITY).
CC -!- SUBUNIT: COMPOSED OF A CATALYTIC SUBUNIT (A) AND A REGULATORY
CC SUBUNIT (B) (BY SIMILARITY).
CC -!- MISCELLANEOUS: THIS PROTEIN HAS FOUR FUNCTIONAL CALCIUM-BINDING
CC SITES (BY SIMILARITY).
CC -!- SIMILARITY: CONTAINS 4 EF-HAND CALCIUM-BINDING DOMAINS.
CC -----
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DR EMBL; AL109850; CAB52879.1; -.
DR HSSP; P06705; LAUI.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR001125; Recoverin.
DR Pfam; PF00036; ehand; 4.
DR PRINTS; PR00450; RECOVERIN.
DR ProDom; PD000012; EF-hand; 1.
DR SMART; SM00054; EFh; 4.
DR PROSITE; PS00018; EF_HAND; 4.
KW Calcium-binding; Myristate.
FT CA_BIND 34 45 EF-HAND 1 (BY SIMILARITY).
FT CA_BIND 66 77 EF-HAND 2 (BY SIMILARITY).
FT FT CA_BIND 103 114 EF-HAND 3 (BY SIMILARITY).
FT FT CA_BIND 144 155 EF-HAND 4 (BY SIMILARITY).
SQ SEQUENCE 174 AA; 19675 MW; EEf38FE74959442E CRC64;

Query Match 19.0%; Score 171.5; DB 1; length 174;
Best Local Similarity 24.4%; Pred. No. 2.1e-09;
Matches 44; Conservative 43; Mismatches 76; Indels 17; Gaps 4;

QY 1 MGSGSRSLSKELLAERYQDLTFLTKQEILLAHRRFCCELLPDQORTVESSLRAQVPFEQILS 60
DB 1 MGQSOSQIFEDLISN---SSFSENEIERIRKRFIK-----IDANQGSIDRNEFLS 48
QY 61 LPELKANPFKERICRVSTSPAKDSLSFEDFLDLSVSDTATPDIKSHYAFRIFXXXXX 120
DB 49 IPSVASNPPLASRLFSVDEDDGGD-VDFQEFINSLSVSFGNKKEKLKFAFKIYDIDRD 107
QY 121 XXXXXXSRVLVNCLTGEGEDTRLASASEMKQLIDNILEESDIDRDGTINLSEFOHVIRS 180
DB 108 GYISNGELYLVLKMMVG----TNLRDQLQQIVDKTIMEYVDKDRDGKISFEFFKDIYSGS 163

RESULT 8
CALB_NEUCR
ID CALB_NEUCR STANDARD; PRT; 174 AA.
AC P87072; O13408;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Calcineurin B subunit (Protein phosphatase 2B regulatory subunit)
DE [Calcineurin regulatory subunit].
GN CNB-1 OR CAN-B.
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=74A;
RX MEDLINE=98007857; PubMed=9349701;
RA Prokisch H., Yarden O., Dleminger M., Tropschug M., Barthelmees I.B.;
RT "Impairment of calcineurin function in Neurospora crassa reveals its
RT essential role in hyphal growth, morphology and maintenance of the
RT apical Ca2+ gradient.";
RL Mol. Genet. Genet. 256:104-114(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=98345933; PubMed=9680955;
RA Kothe G.O., Free S.J.;
RT "Calcineurin subunit B is required for normal vegetative growth in
RT Neurospora crassa.";
RL Fungal Genet. Biol. 23:248-258(1998).
CC -!- FUNCTION: REGULATORY SUBUNIT OF CALCINEURIM, A CALCIUM-DEPENDENT,
CC CALMODULIN STIMULATED PROTEIN PHOSPHATASE. CONFERS CALCIUM
CC SENSITIVITY.
CC -!- SUBUNIT: COMPOSED OF A CATALYTIC SUBUNIT (A) AND A REGULATORY
CC SUBUNIT (B).
CC -!- MISCELLANEOUS: THIS PROTEIN HAS FOUR FUNCTIONAL CALCIUM-BINDING
CC SITES.
CC -!- SIMILARITY: CONTAINS 4 EF-HAND CALCIUM-BINDING DOMAINS.
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DB      1 GAAPSKIYDGLLED-----TNFDRDEIERLRKREMKLDRDSSSGSIDKN-----EFMSI 48
QY      62 PELKANPEKERICRVFSTSPAKDSLSEFEDFLDLSVFSDTATPDIKSHYAFRIEXXXXXX 121
      49 PGVSSNPFLAGRIMEVFADADNSGD-VDFQEFITGLSIFSGRSGKDEKLRFAFKIYDIDKDG 107
QY      122 XXXXXXXXRLVNCITGEGEDTRLASASEMKOLIDNILEESDIDRDGTINLSEFOHVI 177
      108 FINGELLEIVLKIMVG-----SNLDDEQLQOIVDRTIVENDSDGDGRLSFEFEKNAI 159

RESULT 10
CALB_HUMAN
ID      CALB_HUMAN          STANDARD;          PRT;          169 AA.
AC      P06705; P15117; Q08044;
DT      01-JAN-1988 (Rel. 06, Created)
DT      01-APR-1990 (Rel. 14, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      Calcineurin B subunit isoform 1 (Protein phosphatase 2B regulatory
DE      subunit 1) (Protein phosphatase 3 regulatory subunit B alpha isoform
DE      1).
GN      PPP3R1 OR CNB OR CNA2.
OS      Homo sapiens (Human),
OS      Bos taurus (Bovine), and
OS      Rattus norvegicus (Rat).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX      NCBI_TaxID=9606, 9913, 10116;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      SPECIES=Human;
RX      MEDLINE=90126237; PubMed=2558868;
RT      Guerini D., Krinks M.H., Sikela J.M., Hahn W.E., Klee C.B.;
RT      "Isolation and sequence of a cDNA clone for human calcineurin B, the
RT      Ca2+-binding subunit of the Ca2+/calmodulin-stimulated protein
RT      phosphatase.";
RL      DNA 8:675-682(1989).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      SPECIES=Bovine;
RA      Nargang C.E., Bottorff D.A., Adachi K.;
RL      Submitted (APR-1993) to the EMBL/GenBank/DBJ databases.
RN      [3]
RP      SEQUENCE OF 1-168.
RC      SPECIES=Bovine; TISSUE=Brain;
RX      MEDLINE=84132092; PubMed=6321184;
RA      Altken A., Klee C.B., Cohen P.;
RT      "The structure of the B subunit of calcineurin.";
RL      Eur. J. Biochem. 139:663-671(1984).
RN      [4]
RP      SEQUENCE FROM N.A.
RC      SPECIES=Rat;
RA      Perrino B.A., Huang X., Ng L.Y., Soderling T.R.;
RL      Submitted (XXX-1992) to the EMBL/GenBank/DBJ databases.
RN      [5]
RP      SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RC      SPECIES=Rat; TISSUE=Brain, and Testis;
RX      MEDLINE=94153993; PubMed=8110831;
RA      Chang C.-D., Mukai H., Kuno T., Tanaka C.;
RT      "cDNA cloning of an alternatively spliced isoform of the regulatory
RT      subunit of Ca2+/calmodulin-dependent protein phosphatase (calcineurin
RT      B alpha 2).";
RL      Biochim. Biophys. Acta 1217:174-180(1994).
RN      [6]
RP      CALCIUM-BINDING DATA.
RC      SPECIES=Bovine;
RX      MEDLINE=80101597; PubMed=293720;
RA      Klee C.B., Crouch T.H., Krinks M.H.;
RT      "Calcineurin: a calcium- and calmodulin-binding protein of the
RT      nervous system.";
RL      Proc. Natl. Acad. Sci. U.S.A. 76:6270-6273(1979).
RN      [7]
RP      X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).

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RC      SPECIES=Bovine;
RX      MEDLINE=95360994; PubMed=7543369;
RA      Griffith J.P., Kim J.L., Kim E.E., Sintchak M.D., Thomson J.A.;
RA      Fitzgibbon M.J., Fleming M.A., Caron P.R., Hsiao K., Navia M.A.;
RT      "X-ray structure of calcineurin inhibited by the immunophilin-
RT      1 immunosuppressant FKBP12-FK506 complex.";
RL      Cell 82:507-522(1995).
RN      [8]
RP      X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
RC      SPECIES=Human;
RX      MEDLINE=96097077; PubMed=8524402;
RA      Kissinger C.R., Parge H.E., Knighton D.R., Lewis C.T., Pelletier L.A.,
RA      Tempczyk A., Kalish V.J., Tucker K.D., Showalter R.E., Mooney E.W.,
RA      Gastinel L.N., Habuka N., Chen X., Maldonado F., Barker J.E.,
RA      Baquet R., Villafraña J.E.;
RT      "Crystal structures of human calcineurin and the human FKBP12-FK506-
RT      calcineurin complex.";
RL      Nature 378:641-644(1995).
CC      -1- FUNCTION: REGULATORY SUBUNIT OF CALCINEURIN, A CALCIUM-DEPENDENT,
CC      CALMODULIN STIMULATED PROTEIN PHOSPHATASE. CONFERS CALCIUM
CC      SENSITIVITY.
CC      -1- SUBUNIT: COMPOSED OF A CATALYTIC SUBUNIT (A) AND A REGULATORY
CC      SUBUNIT (B).
CC      -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND 2; ARE
CC      PRODUCED BY ALTERNATIVE SPLICING IN RAT.
CC      -1- TISSUE SPECIFICITY: ISOFORM 2 IS TESTIS-SPECIFIC.
CC      -1- MISCELLANEOUS: THIS PROTEIN HAS FOUR FUNCTIONAL CALCIUM-BINDING
CC      SITES.
CC      -1- SIMILARITY: CONTAINS 4 EF-HAND CALCIUM-BINDING DOMAINS.
CC      -----
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CC      or send an email to license@sib-sib.ch).
CC      -----
DR      EMBL; M30773; AAB08721.1; -
DR      EMBL; X71666; CAA50659.1; -
DR      EMBL; I03554; AAA40854.1; -
DR      EMBL; D14568; BAA03422.1; -
DR      EMBL; D14425; BAA03318.1; -
DR      PIR; A33391; A33391.
DR      PIR; S34127; S34127.
DR      PIR; JT0297; JT0297.
DR      PIR; S42716; S42716.
DR      PIR; S42717; S42717.
DR      PDB; 1AUT; 03-DEC-97.
DR      PDB; 1TCO; 12-FEB-97.
DR      Genew; HGNC:9317; PPP3R1.
DR      MIM; 601302; -
DR      InterPro; IPR002048; EF-hand.
DR      Pfam; PF00036; efhand; 4.
DR      ProDom; PD000012; EF-hand; 2.
DR      SMART; SM00054; EFh; 4.
DR      PROSITE; PS00018; EF_HAND; 4.
KW      Calcium-binding; Repeat; Alternative splicing; Myristate;
KW      3D-structure.
FT      INIT_MET 0 0
FT      LIPID 1 1 MYRISTATE.
FT      CA_BIND 30 41 EF-HAND 1.
FT      CA_BIND 62 73 EF-HAND 2.
FT      CA_BIND 99 110 EF-HAND 3.
FT      CA_BIND 140 151 EF-HAND 4.
FT      VARSPLIC 1 1
FT      CONFLICT 11 11
FT      CONFLICT 153 153 C -> M (IN REF. 3).
FT      CONFLICT 153 153 C -> S (IN REF. 3).
SQ      SEQUENCE 169 AA; 19169 MW; 749141BD0434C90C CRC64;
Query Match 16.2%; Score 146.5; DB 1; Length 169;
Best Local Similarity 27.0%; Pred. No. 4.8e-07;

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DR EMBL; AK005067; BAB23791.1; --
DR HSSP; P06705; LAUI.
DR MGD; MGI:1927185; Chp.
DR InterPro; IPR002048; EF-hand.
DR Pfam; PF00036; ehand; 3.
DR ProDom; PD000012; EF-hand; 2.
DR SMART; SM00054; EFh; 2.
DR PROSITE; PS00018; EF_HAND; 1.
KW Calcium-binding; Repeat; Myristate.
FT INIT_MET 0 0
FT LIPID 1 1 MYRISTATE (PROBABLE).
FT DOMAIN 38 49 ANCESTRAL CALCIUM SITE 1 (POTENTIAL).
FT DOMAIN 70 81 ANCESTRAL CALCIUM SITE 2 (POTENTIAL).
FT CA_BIND 122 133 EF-HAND 3 (BY SIMILARITY).
FT CA_BIND 163 174 EF-HAND 4 (BY SIMILARITY).
FT MUTAGEN 133 173 F->A: LOSS OF TARGETING/FUSION FUNCTION.
SQ SEQUENCE 194 AA; 22301 MW; E2DF3E5F627B8231 CRC64;

Query Match 14.9%; Score 135; DB 1; Length 194;
Best Local Similarity 24.2%; Pred. No. 6.9e-06;
Matches 47; Conservative 31; Mismatches 84; Indels 32; Gaps 6;

QY 5 GSR-----LSKELLAEQDITFLTKQEILLAHRRFCELLPQEQRTVSESLRAQVPEGLLS 60
Db 1 GSRASTLLRDEELEIKETGFSHQITRLYSRFTSLDKGNGTLR-----EDFQR 52

QY 61 LPELKANPKERICRVFSTSPAKDSLSFEDFLDLSVF-----SDTATPD----- 105
Db 53 IPELAINPLGDRINAF-FSEGEDQVNFGRFMRTLAHFRPIEDNEKSKDVNGPEPLNSRS 111

QY 106 IKSHYAFRIFFXXXXXXXSRVSLNCLTGEGETRLSASEMKQLIDNILEESDIDRD 165
Db 112 NKLHFAFLYDLKDKKISRDELQLQVLRMVVG-----VNISDEQLGSIADRTIQEADQDGD 167

QY 166 GTINLSEFQHVISR 179
Db 168 SAISFTEFVKVLEK 181

RESULT 14
CALB_DROME STANDARD; PRT; 170 AA.
ID CALB_DROME
AC P48451; Q9W4D0;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Calcineurin B subunit, isoform 1 (Protein phosphatase 2B regulatory subunit).
GN CANB OR CANB1 OR CNB1 OR CNB OR CG4209.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93054551; PubMed=1331060;
RA Guerini D., Montell C., Klee C.B.;
RT "Molecular cloning and characterization of the genes encoding the two subunits of Drosophila melanogaster calcineurin.";
RL J. Biol. Chem. 267:22542-22549(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
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RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Fosler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhou W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
CC -!- FUNCTION: CALCINEURIN IS A CALCIUM BINDING AND CALMODULIN BINDING
CC PROTEIN FOUND IN ALL CELLS FROM YEAST TO MAMMALS, IT IS A CALCIUM
CC DEPENDENT, CALMODULIN STIMULATED PROTEIN PHOSPHATASE (BY
CC SIMILARITY).
CC -!- SUBUNIT: COMPOSED OF TWO COMPONENTS (A AND B), THE A COMPONENT IS
CC THE CATALYTIC SUBUNIT AND THE B COMPONENT CONFERS CALCIUM
CC SENSITIVITY (BY SIMILARITY).
CC -!- MISCELLANEOUS: THIS PROTEIN HAS FOUR FUNCTIONAL CALCIUM-BINDING
CC SITES.
CC -!- SIMILARITY: TO OTHER EF-HAND CALCIUM BINDING PROTEINS.
CC -----
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CC -----
CC EMBL; M97215; AAA28411.1; --
CC EMBL; AE003434; AAF46026.1; --
CC HSSP; P06705; ITCO.
CC FlyBase; FBgn0010014; CanB.
CC InterPro; IPR002048; EF-hand.
CC Pfam; PF00036; ehand; 4.
CC ProDom; PD000012; EF-hand; 2.
CC SMART; SM00054; EFh; 4.
CC PROSITE; PS00018; EF_HAND; 4.
KW Calcium-binding; Repeat.
FT CA_BIND 31 42 EF-HAND 1 (POTENTIAL).
FT CA_BIND 63 74 EF-HAND 2 (POTENTIAL).
FT CA_BIND 100 111 EF-HAND 3 (POTENTIAL).
FT CA_BIND 141 152 EF-HAND 4 (POTENTIAL).
SQ SEQUENCE 170 AA; 19341 MW; 77D89BE9BD961900 CRC64;

Query Match 14.7%; Score 132.5; DB 1; Length 170;
Best Local Similarity 23.2%; Pred. No. 1e-05;
Matches 36; Conservative 34; Mismatches 72; Indels 13; Gaps 3;

QY 26 EILLAHRRFCELLPQEQRTVSESLRAQVPEGLLSLPKANKPKERICRVFSTSPAKDS 85
Db 19 EIRRLGKRF-----RKLDLDNSGALSIDFMSLPQLQNPLVQRVIDIFD-ADNGNE 69
```

QY 86 LSFEDLDLVSFSDTATPDIKSHVAFRIEXXXXXXXXSRVNCLTGEGEDTRL 145
Db 70 VDFKERTIGVSOFSVRGDKLSKLRFAFRIFYDMNDGYISNGELFQVLKMYG----NMLK 125
QY 146 ASEMQLIDNILESDIDRDGTINLSEFQHVISR 180
Db 126 DTOLQIVDKTICFADKDEDGKISFDEFCSVVGNT 160

RESULT 15
CA22_HUMAN
ID CA22_HUMAN STANDARD; PRT; 194 AA.
AC Q99653.
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Calcium-binding protein p22 (Calcium-binding protein CHP) (Calcineurin homologous protein) (Calcineurin B homolog).
GN CHP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=B-cell;
RX MEDLINE-97057295; PubMed-8901634;
RA Lin X., Barber D.L.;
RT "A calcineurin homologous protein inhibits GTPase-stimulated Na-H exchange."
RL Proc. Natl. Acad. Sci. U.S.A. 93:12631-12636(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Muscle;
RA Strausberg R.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: REQUIRED FOR CONSTITUTIVE MEMBRANE TRAFFIC (BY SIMILARITY). INHIBITS GTPASE-STIMULATED NA-H EXCHANGE.
CC SPECIFICALLY BINDS TO THE SODIUM/HYDROGEN EXCHANGER 1 (NHE1) AT A DOMAIN THAT IS CRITICAL FOR GROWTH FACTOR STIMULATION OF EXCHANGE ACTIVITY.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- TISSUE SPECIFICITY: UBIQUITOUSLY EXPRESSED. HAS BEEN FOUND IN FETAL EYE, LUNG, LIVER, MUSCLE, HEART, KIDNEY, THYMUS AND SPLEEN.
CC -1- PTM: BOTH N-MYRISTOYLATION AND CALCIUM-MEDIATED CONFORMATIONAL CHANGES ARE ESSENTIAL FOR ITS FUNCTION IN EXOCYTIC TRAFFIC (BY SIMILARITY).
CC -1- PTM: PHOSPHORYLATED IN VIVO. DECREASE IN ITS PHOSPHORYLATION IS ASSOCIATED WITH AN INCREASE IN EXCHANGE ACTIVITY. THE PHOSPHORYLATION STATE MAY REGULATE THE BINDING TO NHE1.
CC -1- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
CC -----
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CC -----
DR EMBL; U61538; AAB37770.1; .
DR EMBL; BC001646; AAH01646.1; .
DR HSSP; P06705; 1AUI.
DR MIM; 606988; .
DR InterPro; IPR002048; EF-hand.
DR Pfam; PF00036; efhand; 3.
DR ProDom; PD000012; EF-hand; 2.
DR SMART; SM00054; EFh; 2.
DR PROSITE; PS00018; EF_HAND; FALSE_NEG.
KW Calcium-binding; Repeat; Myristate; Phosphorylation.
FT INIT_MET 0
FT LIPID 1
FT DOMAIN 38 49 MYRISTATE (BY SIMILARITY).
ANCESTRAL CALCIUM SITE 1 (POTENTIAL).

FT DOMAIN 70 81 ANCESTRAL CALCIUM SITE 2 (POTENTIAL).
FT CA_BIND 122 133 EF-HAND 3 (BY SIMILARITY).
FT CA_BIND 163 174 EF-HAND 4 (BY SIMILARITY).
SQ SEQUENCE 194 AA; 22325 MW; 17DDEE5F03C88380 CRC64;
Query Match 14.5%; Score 131; DB 1; Length 194;
Best Local Similarity 23.7%; Pred. No. 1.7e-05;
Matches 46; Conservative 31; Mismatches 85; Indels 32; Gaps 6;
QY 5 GSR----LSKELLA EYQDLTFLTKQELILAHRRFCCELLPOEQRTVESSLRAQVPFEQILS 60
Db 1 GSRASTLLRDEDELEIEIKKETGFSHQITRLYSRFTSLDKGNGTLR-----EDFOR 52
QY 61 LPELKANPKEKRICRVFSTSPAKDSLSFEDLDLSVF-----SDTATPD----- 105
Db 53 IPELAINPLGDRITINAFPE-GEQVNRFGFMRTLAHFRPIEDNEKSKDVNGPEPLNSRS 111
QY 106 IKSHVAFRIEXXXXXXXXSRVNCLTGEGEDTRLASSEMQLIDNILESDIDRD 165
Db 112 NKLHFAFRXYDLDKDEKISRDELLQVLRMYG----VNISDEGLSIADRTIQEADQDGD 167
QY 166 GTINLSEFQHVISR 179
Db 168 SAISFTEFYKYLEK 181

Search completed: January 17, 2003, 12:45:50
Job time : 13 secs

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OM protein - protein search, using sw model

Run on: January 17, 2003, 12:43:58 ; Search time 31 Seconds

(without alignments)
1269.516 Million cell updates/sec

Title: US-09-878-454A-2X

Perfect score: 904
Sequence: 1 MGSGSRLSKELLAEXQDLT.....EFQHVISRSPDFASSFKIVL 191

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriaph:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	367	40.6	311	5	Q93640	Q93640 caenorhabdi
2	318	35.2	185	11	Q9D9N5	Q9d9n5 mus musculu
3	310	34.3	187	4	Q96077	Q96q77 homo sapien
4	297.5	32.9	206	5	Q9W2Q5	Q9w2q5 drosophila
5	194	21.5	54	6	Q9GLJ2	Q9glj2 sus scrofa
6	188.5	20.9	180	5	Q9GP83	Q9gp83 dictyosteli
7	161	17.8	175	10	Q93VF2	Q93vf2 eucalyptus
8	161	17.8	175	10	Q9LS47	Q9ls47 arabidopsis
9	159	17.6	175	5	Q9U0X7	Q9u0x7 leishmania
10	144.5	16.0	169	5	Q9NFM1	Q9nfm1 schistosoma
11	144.5	16.0	244	5	Q20804	Q20804 caenorhabdi
12	140.5	15.5	170	5	Q9NKM7	Q9nkm7 patinopecte
13	140.5	15.5	195	5	Q23643	Q23643 caenorhabdi
14	140	15.5	29	11	Q99JY5	Q99jy5 mus musculu
15	139.5	15.4	213	5	O16343	O16343 caenorhabdi
16	138.5	15.3	170	5	O95P81	O95p81 bombyx mori

17	137.5	15.2	115	11	Q99LQ9	Q99lq9 mus musculu
18	137	15.2	274	10	Q9AMW4	Q9aww4 oryza sativ
19	136	15.0	200	5	Q8SRF8	Q8srif8 encephalito
20	134	14.8	214	11	Q8VCN1	Q8vcn1 mus musculu
21	133.5	14.8	213	10	Q9LTB8	Q9ltb8 arabidopsis
22	132.5	14.7	175	3	Q9HDE1	Q9hde1 cryptococcu
23	132.5	14.7	177	3	Q9HDD3	Q9hdd3 cryptococcu
24	130.5	14.4	226	10	O81446	O81446 arabidopsis
25	130	14.4	170	4	Q8WYJ4	Q8wyj4 homo sapien
26	130	14.4	173	4	Q96LZ3	Q96l23 homo sapien
27	127	14.0	216	4	Q9NWT9	Q9nwt9 homo sapien
28	126.5	14.0	161	10	Q9AY39	Q9ay39 oryza sativ
29	126.5	14.0	187	5	Q9VWX8	Q9vwx8 drosophila
30	124.5	13.8	189	5	Q9VNF9	Q9vnf9 drosophila
31	122	13.5	190	3	Q96X50	Q96x50 magnaporthe
32	122	13.5	190	3	Q8TGC0	Q8tgc0 magnaporthe
33	121	13.4	191	4	Q9UM19	Q9um19 homo sapien
34	121	13.4	192	10	O81328	O81328 arabidopsis
35	120	13.3	225	10	O8W5C8	O8w5c8 oryza sativ
36	119	13.2	196	5	Q9N2Y1	Q9n2y1 caenorhabdi
37	118.5	13.1	226	10	O81447	O81447 arabidopsis
38	117	12.9	246	10	O82641	O82641 arabidopsis
39	114.5	12.7	213	10	O81445	O81445 arabidopsis
40	112	12.4	190	5	Q9NAY9	Q9nay9 naegleria f
41	111	12.3	214	10	Q9FUQ7	Q9fuq7 arabidopsis
42	111	12.3	222	10	O81223	O81223 arabidopsis
43	111	12.3	224	10	Q9SGW7	Q9sgw7 arabidopsis
44	110.5	12.2	153	5	Q9U5J0	Q9u5j0 trichomonas
45	110.5	12.2	160	5	Q9U5I9	Q9u5i9 trichomonas

ALIGNMENTS

RESULT 1	
Q93640	PRELIMINARY; PRT; 311 AA.
ID	Q93640;
AC	Q93640;
DT	01-FEB-1997 (Tremblrel. 02, Created)
DT	01-FEB-1997 (Tremblrel. 02, Last sequence update)
DT	01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE	F30A10.1 protein.
GN	F30A10.1.
OS	Caenorhabditis elegans.
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC	Rhabditidae; Peloderinae; Caenorhabditis.
OX	NCBI_TaxID-6239;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	Barlow X.;
RL	Submitted (OCR-1996) to the EMBL/GenBank/DBJ databases.
RN	[2]
RP	SEQUENCE FROM N.A.
RA	MEDLINE-99069613; PubMed-9851916;
RT	none;
RT	"Genome sequence of the nematode C.elegans: A platform for
RL	Investigating biology.";
RL	Science 282:2012-2018(1998).
DR	EMBL; 281072; CAB03019.1; -
DR	HSSP; Q99828; 1DGv.
DR	InterPro; IPR002048; EF-hand.
DR	Pfam; PF00036; efhand; 3.
DR	ProDom; PD000012; EF-hand; 1.
DR	SMART; SM00054; EFh; 2.
DR	SEQUENCE . 311 AA; 35960 MW; 97AFOAF56A6F526F CRC64;
QY	Query Match 40.6%; Score 367; DB 5; Length 311;
QY	Best Local Similarity 39.6%; Pred. No. 3.4e-30;
QY	Matches 82; Conservative 39; Mismatches 60; Indels 26; Gaps 5;
Db	111 MGNASSLSLEINLFSGKGVFTREQLDEYQDCTFTTRKIDIRLYKRYALNPHK---VPTN 167


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RC STRAIN-BERKELEY;
RX MEDLINE-20196006; PubMed-10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Bailew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
RA Butlis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrieri S., Fleischmann W.,
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirska R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
DR EMBL; AE003452; AAF46635.1; -
DR HSSP; Q99828; IDGV.
DR FLYBase; FBgn0034558; CG9236.
DR InterPro; IPR002048; EF-hand.
DR Pfam; PF00036; efhand; 3.
DR ProDom; PD000012; EF-hand; 1.
DR SMART; SM00054; EFh; 3.
DR PROSITE; PS00018; EF_HAND; 2.
KW Calcium-binding.
SQ SEQUENCE 206 AA; 23591 MW; B3105FF7F0F475A9 CRC64;

Query Match 32.9%; Score 297.5; DB 5; Length 206;
Best Local Similarity 40.9%; Pred. No. 3.8e-23;
Matches 72; Conservative 30; Mismatches 57; Indels 17; Gaps 5;

OY 17 QDLFLTKQELLAHRRFCELLPQ--EQRTVESSLRAQVPFEQILSLPELKANPFKERI 73
Db 43 KDCFTFTKREILRVHKKRRELRLPDLVPRQMTGQASSVKVPCECIKMPDLR----- 94

OY 74 CRVESTPAKDSLSFEDFLDLVSFSDTATPDIKSHYAFRIFFXXXXXXXSRLLVN 133
Db 95 -EAFSRD-GQGNLSFEDFLDALVSFEQAPRDIKVFYAFKIY--DFDQDGFIGHADLMS 149

OY 134 CLTGEEDTRLASSEMQLIDNILESDIDRDGTINLSEFQHVISRSPDEASSFKI 189
Db 150 CLTMTKKN-ELSPHEHQIADKVIKVEADVDGDKLSLFEFHVILRADPFLSTFHI 204

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DT 01-MAR-2001 (Tremblrel. 16, last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, last annotation update)
DE DNA-PK interaction-like protein (Fragment).
OS Sus scrofa (pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Smith T.P.L., Fahrenkrug S.C., Rohrer G.A., Simmen F.A.,
RA Rexroad C.E. III, Keele J.W.;
RT "Mapping of Expressed Sequence Tags from a porcine early embryonic
RT cDNA library.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF267715; AAG25931.1; -
DR HSSP; Q99828; IDGV.
DR InterPro; IPR002048; EF-hand.
DR Pfam; PF00036; efhand; 1.
DR ProDom; PD000012; EF-hand; 1.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
FT NON_TER 1
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 54 AA; 6107 MW; 1A8057DE68A57A4A CRC64;

Query Match 21.5%; Score 194; DB 6; Length 54;
Best Local Similarity 74.1%; Pred. No. 4.9e-13;
Matches 40; Conservative 1; Mismatches 13; Indels 0; Gaps 0;

OY 102 ATPDIKSHYAFRIFFXXXXXXXSRVNCLTGEGEDTRLASSEMQLIDN 155
Db 1 ATPDIKSHYAFRIFFDDDDGTLNRDLSQLVNCLTGEEDTRLASSEMQLIDN 54

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RESULT 6
OY 09GP83 PRELIMINARY; PRT; 180 AA.
AC 09GP83;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-JUN-2001 (Tremblrel. 17, last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, last annotation update)
DE Calcineurin B.
GN CNBA.
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyostellida; Dictyostellium.
OX NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-AX-2;
RA Alchem A.;
RL Thesis (2000), Department of Fachbereich Biologie,
RL Universitaet Konstanz, Konstanz, Germany.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-AX-2;
RA Alchem A.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ301668; CAC20026.2; -
DR HSSP; P06705; LAUI.
DR InterPro; IPR002048; EF-hand.
DR Pfam; PF00036; efhand; 4.
DR PRINTS; PR00450; RECOVERIN.
DR ProDom; PD000012; EF-hand; 2.
DR SMART; SM00054; EFh; 4.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_3.
SQ SEQUENCE 180 AA; 20739 MW; E2E947E8D280D0B6 CRC64;

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Query Match 20.9%; Score 188.5; DB 5; Length 180;
Best Local Similarity 27.0%; Pred. No. 8.3e-12;
Matches 48; Conservative 41; Mismatches 74; Indels 15; Gaps 4;

OY 1 MGSGSRLSKELLAAYQDLFLTKQELLAHRRFCELLPQEQRTVESSLRAQVPFEQILS 60

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Db 1 MGNHSLNKEQLEQMDKNSFSEAEKLYRRFQMLDKDGSGLTT-----DEFLS 52

QY 61 LPELKANPFKERICRVFSTSPAKDS-LSFEDFLDLLSVFSDTATPDIKSHYAFRIFXXXX 119

Db 53 IPDLALNPLLERVIQFDQN--KDNEIEFSEFVGTATLSHGKTKEDKLKFLQIYDIDC 110

QY 120 XXXXXXXXXXSRVLNCLTGEGETRLSASEMKQLIDNILEESDIDRDGTINLSEFQHV 177

Db 111 DGFISNGELFQVLKMMVG-----TNLNDVQLQIIVDKTIIEGDYDKDGKISFDEFIHM 164

RESULT 7

Q93VF2

ID Q93VF2 PRELIMINARY; PRT; 175 AA.

AC Q93VF2;

DT 01-DEC-2001 (TREMBlrel. 19, Created)

DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)

DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)

DE Calcineurin-like protein.

GN ECCBL1-OR EGCBL1.

OS Eucalyptus camaldulensis (Murray red gum), and

OS Eucalyptus grandis.

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC eurosids II; Myrtales; Myrtaceae; Eucalyptus.

OX NCBI_TaxID=34316, 71139;

RN [1]

RP SEQUENCE FROM N.A.

RC SPECIES=E.camaldulensis, and E.grandis; TISSUE=FLOWER;

RA Fairbairn D.J., Gomez-Gallego S., Sawbridge T., Teasdale R.D.;

RL Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.

DR EMBL; AF197334; AAL25650.1; -.

DR EMBL; AF197330; AAL25647.1; -.

DR InterPro; IPR002048; EF-hand.

DR Pfam; PF00036; efhand; 2.

DR ProDom; PD000012; EF-hand; 1.

DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.

DR SEQUENCE 175 AA; 19997 MW; C4E773EE42A3EF16 CRC64;

Query Match 17.8%; Score 161; DB 10; Length 175;

Best Local Similarity 24.2%; Pred. No. 6.1e-09;

Matches 44; Conservative 41; Mismatches 77; Indels 20; Gaps 4;

QY 1 MGGSGSRLSKELLAEQD--LTFLTKQEILLAHRRFCELLPQEORTVLESSLRAQVPFEQI 58

Db 1 MGNASSMLTQYDIEEVQDHCNNLFSQQEIVSLYERFCQL-----DRNAKGFISADEF 52

QY 59 LSLPELKANPFKERICRVFSTSPAKDSLSFEDFLDLLSVFSDTATPDIKSHYAFRIFXXX 118

Db 53 LSVPEFAMNPLSQRLKLV-----DGLNFKDFVAFLSAFSAKASKQKQKIELIFKVIDSD 106

QY 119 XXXXXXXXXXSRVLNCLTGEGETRLSASEMKQLIDNILEESDIDRDGTINLSEFQHV 178

Db 107 CNGKVSFNDILEVLRDLG----PFMSDEQREQLVQLVKEAGYTRESYLLLDLDFVKVFG 162

QY 179 RS 180

Db 163 NS 164

RESULT 8

Q9LS47

ID Q9LS47 PRELIMINARY; PRT; 175 AA.

AC Q9LS47;

DT 01-OCT-2000 (TREMBlrel. 15, Created)

DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)

DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)

DE Calcineurin b subunit (Protein phosphatase 2b regulatory subunit)-like

DE protein (Hypothetical 20.0 kDa protein).

GN AT3G18430.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.

OX NCBI_TaxID=3702;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=COLUMBIA;

RA Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata S.;

RL Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=COLUMBIA;

RX MEDLINE=20277480; PubMed=10819329;

RA Nakamura Y.;

RT "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence

RT features of the regions of 4,504,864 bp covered by sixty P1 and TAC

RT clones.";

RL DNA Res. 7:131-135(2000).

RN [3]

RP SEQUENCE FROM N.A.

RA Yamada K., Banh J., Banno F., Chang E., Dale J.M., Goldsmith A.D.,

RA Lee J.M., Onodera C.S., Quach H.L., Tang C., Toriumi M., Wu H.C.,

RA Yamamura Y., Yu G., Yu S., Bowser L., Carrinci P., Chen H., Cheuk R.,

RA Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,

RA Kawai J., Kim C., Koesema E., Lam B., Lin J., Meyers M.C., Miranda M.,

RA Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M.,

RA Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,

RA Theologis A.;

RT "Full Length cDNA of gene At3g18430 (GI:15229640).";

RL Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.

RN [4]

RP SEQUENCE FROM N.A.

RA Yamada K., Banh J., Chan M.M., Chang C.H., Chang E., Dale J.M.,

RA Deng J.M., Goldsmith A.D., Lee J.M., Onodera C.S., Quach H.L.,

RA Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bowser L.,

RA Carrinci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,

RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,

RA Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J.,

RA Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Shinozaki K.,

RA Davis R.W., Ecker J.R., Theologis A.;

RT "Arabidopsis Open Reading Frame (ORF) Clones.";

RL Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.

DR EMBL; AB026658; BAB01109.1; -.

DR EMBL; AY063789; AAL36096.1; -.

DR EMBL; AY091287; AAM14226.1; -.

DR HSSP; P06705; 1AUI.

DR InterPro; IPR002048; EF-hand.

DR Pfam; PF00036; efhand; 2.

DR ProDom; PD000012; EF-hand; 1.

DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.

KW Hypothetical protein.

SQ SEQUENCE 175 AA; 20032 MW; B26D6F2ADA26AFED CRC64;

Query Match 17.8%; Score 161; DB 10; Length 175;

Best Local Similarity 25.0%; Pred. No. 6.1e-09;

Matches 46; Conservative 40; Mismatches 74; Indels 24; Gaps 5;

QY 1 MGGSGSRLSKELLAEQD--LTFLTKQEILLAHRRFCELLPQEORTVLESSLRAQVPFE 56

Db 1 MGNASSMLTQYDIEEVQSHCHDL--FEQOEILSLYQRFQCL-----DRNAKGFISAD 50

QY 57 QILSLPELKANPFKERICRVFSTSPAKDSLSFEDFLDLLSVFSDTATPDIKSHYAFRIFX 116

Db 51 EFLSVPEFAMNPLSQRLKLV-----DGLNFKDFVAFLSAFSAKASLRQKVLIFKVID 104

QY 117 XXXXXXXXXXSRVLNCLTGEGETRLSASEMKQLIDNILEESDIDRDGTINLSEFQHV 176

Db 105 SDCNGKVSFKDIMEVLRDLG----SFMSDEQREQLVSLKESGYTSDSFLTLEDFIKI 160

QY 177 ISRS 180

Db 161 FGSS 164

RESULT 9

Q9U0X7
ID Q9U0X7 PRELIMINARY; PRT; 175 AA.
AC Q9U0X7;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Calciueurin subunit.
GN L7171.06.
OS Leishmania major.
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID=5664;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-FRIEDLIN;
RA Tosato V., Bruschi C.V., Iyens A.C., Murphy L., Quall M.,
RA Rajandream M.A., Barrell B.G.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-FRIEDLIN;
RX MEDLINE=98146435; PubMed=9477341;
RA Iyens A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M.,
RA Smith D.F.;
RT "A physical map of the leishmania major Friedlin genome.";
RL Genome Res. 8:135-145(1998).
DR EMBL, AL133435; CAB62809.1; -
DR HSSP; P06705; 1AUI.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR001125; Recoverin.
DR Pfam; PF00036; efhand; 4.
DR PRINTS; PR00450; RECOVERIN.
DR ProDom; PD000012; EF-hand; 2.
DR SMART; SM00054; EFh; 3.
DR POSITE; PS00018; EF_HAND; UNKNOWN 2.
SO SEQUENCE. 175 AA; 19660 MW; 9448F127E4DFA0EB CRC64;

Query Match	17.6%	Score 159;	DB 5;	Length 175;
Best Local Similarity	22.5%	Pred. No. 9.9e-09;		
Matches 41; Conservative	41;	Mismatches 86;	Indels 14;	Gaps 4;

[illegible]

RA C1011 D., Klinkert M.O.;
RT "Molecular cloning of Schistosoma mansoni calcineurin subunits and
RT Immunolocalization to the excretory system.",
RL Mol. Biochem. Parasitol. 110:333-343(2000).
DR EMBL; AJ276885; CAB93677.1; -.
DR HSSP; P06705; LTCO.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR001125; Recoverin.
DR Pfam; PF00036; ehand; 4.
DR PRINTS; PR00450; RECOVERIN.
DR ProDom; PD000012; EF-hand; 2.
DR SMART; SM00054; EFh; 4.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_4.
SO SEQUENCE 169 AA; 19137 MW; 878E01D08BC5DC1D CRC64;

Query Match	16.08;	Score 144.5;	DB 5;	Length 169;
Best Local Similarity	26.08;	Pred. No. 3.1e-07;		
Matches 32; Conservative	29;	Mismatches 57;	Indels 5;	Gaps 2;

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QY 56 EQLSLPELKANPEKERICRVSTSPAKDSLSFEDELDDLVSFSDTATPDIKSHYAFRIE 115
   :::||||: || |::: ||::: || || |::|:
Db 40 KEFMSLPQLQNDLVARVIEIFDTD-GNGEYDFKEFINGMSQFSKAGEKAKLKFAFKIY 98
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QY 116 XXXXXXXXXXXXSRVNLCTGEGEDTRISASEMKOLIDNILEESDIDRGDTINLSEFQH 175
      :: : | : ::::: : | | | | : ||
Db 99 DMDKDYISNGEQLVLMVVG---NNLKDQTOLQQIVDKTIMPPDKDEDEGRISFEFCE 154
```

QY	176	VIS	178
		1:1	
Db	155	VVS	157

RESULT 11
Q20804

ID	Q20804	PRELIMINARY;	PRT;	244	AA.
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DT	01-NOV-1996	(TREMBLrel. 01, Created)
DT	01-MAY-2000	(TREMBLrel. 13, Last sequence update)
DT	01-MAR-2002	(TREMBLrel. 20, Last annotation update)
DE	F55C10.1 protein.	

0S *Caenorhabditis elegans*.
0C Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
0C Rhabditidae; Peloderinae; Caenorhabditis.
0X NCBI_TaxID=6239;

RP SEQUENCE FROM N.A.
RA Dobson R.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.

RP SEQUENCE FROM N.A.
RX MEDLINE-99069613; PubMed-9851916;

"Genome sequence of the nematode *C.elegans*: A platform for

RT Investigating biology.";
RL Science 282:2012-2018(1998).
DR EMBL; Z74036; CAA98489.2; -.

```
DR InterPro; IPR002048; EF-hand.  
DR InterPro; IPR001125; RecoverIn.  
DR InterPro; IPR001125; RecoverIn.
```

DR PRINTS; PR00450; RECOVERIN.
DR ProDom; PD000012; EF-hand; 2

```
DR PROSITE; PS00018; EF_HAND; UNKNOWN_4.  
SQ SEQUENCE 244 AA; 27901 MW; 6B99CB58CB77D08B CRC64;
```

Query Match	16.0%;	Score 144.5;	DB 5;	Length 244;
Best Local Similarity	25.0%;	Pred. No. 4.9e-07;		
Matches 45;	Conservative 35;	Mismatches 77;	Indels 23;	Gaps 6

QY 3 GSGSRLSKELLAEQ--DITFLTQKEILLAHRCCELLPQORTVESSTRAQVEEQILS 60
| : : | : : : : | | | | : | : : : |

Db 75 GADASLPMEMCSNFDAYELRLT-----RRFKKL-----DVGDS--GSLSVEEFMS 118

QY 61 LPELKANPFKERICRVFSTSPAKDSLSFEDFLDLLSVFSDTATPDIKSHYAFRIFXXXXX 120

Db 119 LPELQONPLVQRVIDIFD-EDNGEVDFFEFIQISQFSVKGDKNTKLKFAFRIYDMDRD 177

QY 121 XXXXXXSRLVNLCTGEGEDTRLSASEMKQLIDNILEESDIDRGTINLSEFQHVIRS 180

Db 178 GFISNGELFQVLKMWVG----NNLKDSQLQIIVDKTILFHDKDGDKISFQEFCDVVEHT 233

RESULT 12

Q9NWK7

ID Q9NWK7 PRELIMINARY; PRT; 170 AA.

AC Q9NWK7;

DT 01-OCT-2000 (TremBLrel. 15, iCreated)

DT 01-OCT-2000 (TremBLrel. 15, Last sequence update)

DT 01-JUN-2002 (TremBLrel. 21, Last annotation update)

DE Calcineurin B.

OS Patinopecten yessoensis (Ezo giant scallop) (Yesso scallop).

OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Pectinoidea;

OC Pectinoidea; Pectinidae; Mizuhopecten.

OX NCBI_TaxID=6573;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=TESTIS;

RA Uryu M., Nakatomi A., Watanabe M., Hatsuse R., Yazawa M.;

RT "Molecular Cloning of cDNA Encoding Two Subunits of Calcineurin from Scallop Testis: Demonstration of Stage-Specific Expression during Maturation of the Testis";

RL J. Biochem. 0:0-0(2000).

DR EMBL; AB041524; BAA94543.1; -.

DR HSSP; P06705; IAU1.

DR InterPro; IPR002048; EF-hand.

DR InterPro; IPR001125; Recoverin.

DR Pfam; PF00036; ehand; 4.

DR PRINTS; PR00450; RECOVERIN.

DR ProDom; PD000012; EF-hand; 2.

DR SMART; SM00054; EFh; 4.

DR PROSITE; PS00018; EF_HAND; UNKNOWN_4.

SQ SEQUENCE 170 AA; 19238 MW; 9450322698470F44 CRC64;

Query Match 15.5%; Score 140.5; DB 5; Length 170;

Best Local Similarity 22.3%; Pred. No. 8.2e-07;

Matches 39; Conservative 39; Mismatches 78; Indels 19; Gaps 4;

QY 3 GSGSRLSKELLAAYQDLTFLTKQEILLAHRRFCELLPQEQRTVSSSLRAQVPFEQILSLP 62

Db 2 GNENSLPMLCSNFD-----PDEIKRLGKRF-----RKLDLNSGSLSVDEFMTLP 47

QY 63 ELKANPFKERICRVFSTSPAKDSLSFEDFLDLLSVFSDTATPDIKSHYAFRIFXXXXXX 122

Db 48 ELQONPLVQRVIDIFD-EDNGEVDFFEFIEGVSQFSVKGDKLSKLRFKFIYDMDKDGY 106

QY 123 XXXXXXSRLVNLCTGEGEDTRLSASEMKQLIDNILEESDIDRGTINLSEFQHVI 177

Db 107 ISNGELFQVLKMWVG----NNLKDTQLQIIVDKTIIHADADGDKISFEFCVV 157

RESULT 13

Q23643

ID Q23643 PRELIMINARY; PRT; 195 AA.

AC Q23643;

DT 01-NOV-1996 (TremBLrel. 01, Created)

DT 01-NOV-1996 (TremBLrel. 01, Last sequence update)

DT 01-MAR-2002 (TremBLrel. 20, Last annotation update)

DE ZK856.8 protein.

GN ZK856.8.

OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;

OC Rhabditidae; Peloderinae; Caenorhabditis.

OX NCBI_TaxID=6239;

RN [1]

RP SEQUENCE FROM N.A.

RA Lloyd C.R.;

RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=99069613; PubMed=9851916;

RA none;

RT "Genome sequence of the nematode C.elegans: A platform for investigating biology.";

RL Science 282:2012-2018(1998).

DR EMBL; Z70783; CAA94856.1; -.

DR HSSP; P06705; IAU1.

DR InterPro; IPR002048; EF-hand.

DR Pfam; PF00036; ehand; 3.

DR ProDom; PD000012; EF-hand; 2.

DR SMART; SM00054; EFh; 2.

DR PROSITE; PS00018; EF_HAND; UNKNOWN_2.

SQ SEQUENCE 195 AA; 22670 MW; 9F4FDD6D8BD7BA88 CRC64;

Query Match 15.5%; Score 140.5; DB 5; Length 195;

Best Local Similarity 22.3%; Pred. No. 9.8e-07;

Matches 44; Conservative 40; Mismatches 82; Indels 31; Gaps 6;

QY 1 MGGSGS-RLSKELLAAYQDLTFLTKQEILLAHRRFCELLPQEQRTVSSSLRAQVPFEQIL 59

Db 1 MGNSSSLMRDEEIEEIMSETEFNRNQIVRLSYRFLSLDKKGQGLSR-----DDFL 52

QY 60 SLPELKANPFKERICRVFSTSPA-----KDSLSFEDFLDLLSVFSDTATPDIKSH---- 109

Db 53 NPVELAVNPLGDRIVDAFFTLASSNGDNEEQQLNFRQFVRILAHFQPISR--VKKNALNS 110

QY 110 -----YAFRIFXXXXXXXSRLVNLCTGEGEDTRLSASEMKQLIDNILEESDID 163

Db 111 RKDKLLFAFKMYDLNKNNDYITREEFKVILNSMVG----ANITSDQLDKIADRTIEADAD 166

QY 164 RDGTINLSEFQHVIRS 180

Db 167 RDGKISFDEFCEKAMEKT 183

RESULT 14

Q99JY5

ID Q99JY5 PRELIMINARY; PRT; 29 AA.

AC Q99JY5;

DT 01-JUN-2001 (TremBLrel. 17, Created)

DT 01-JUN-2001 (TremBLrel. 17, Last sequence update)

DT 01-JUN-2002 (TremBLrel. 21, Last annotation update)

DE Similar to protein kinase, DNA activated, catalytic polypeptide interacting protein.

DE Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RA Strausberg R.;

RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC005570; AAH05570.1; -.

DR HSSP; Q99828; IDGV.

KW Kinase.

SQ SEQUENCE 29 AA; 3242 MW; E19D6177AF420612 CRC64;

Query Match 15.5%; Score 140; DB 11; Length 29;

Best Local Similarity 100.0%; Pred. No. 1e-07;

Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGGSGSRLSKELLAAYQDLTFLTKQEILL 29

Db 1 MGGSGSRLSKELLAAYQDLTFLTKQEILL 29

RESULT 15

O16343


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XX WPI; 1998-240018/21.
XX N-PSDB; AAV07211.
XX
XX PT New isolated calcium-integrin binding protein - is expressed in
XX PT platelets and activates the fibrinogen receptor, used to develop
XX PT products for treating e.g. vascular disorders
XX
XX Claim 1; Page 30; 44pp; English.
XX
XX CC This is the amino acid sequence of the human calcium-integrin binding
XX CC (CIB) protein, that binds to the integrin alpha IIB cytoplasmic
XX CC domain. The CIB protein is expressed in platelets and interacts with
XX CC the alpha IIB subunit of integrin alpha IIB-beta 3, to activate the
XX CC fibrinogen receptor. Inhibitory compounds can be used to inhibit the
XX CC activation of the fibrinogen-receptor where it is desired to reduce
XX CC blood coagulation for therapeutic, diagnostic or pharmaceutical
XX CC reasons. The products can be used for treating vascular disorders,
XX CC and for isolating or purifying integrins or fibrinogen. They can also
XX CC be used for detection and diagnosis.
XX
XX Sequence 191 AA;
XX
XX Query Match          99.6%; Score 900; DB 19; Length 191;
XX Best Local Similarity 92.7%; Pred. NO. 1.6e-81;
XX Matches 177; Conservative 14; Mismatches 0; Indels 0; Gaps 0;
XX
QY      1  MGSGSRLSKELLAEQDLTFLTKQEILLAHRRFCELLPQEQSVESSLRAQVPFEQLS 60
Db      1  MGSGSRLSKELLAEQDLTFLTKQEILLAHRRFCELLPQEQSVESSLRAQVPFEQLS 60
QY     61  LPELKANPFKEICRVFSTSPAKDSLSFEDFLDLSVFSPTATPDIKSHYAFRIFXXXXX 120
Db     61  LPELKANPFKEICRVFSTSPAKDSLSFEDFLDLSVFSPTATPDIKSHYAFRIFDFDDD 120
QY    121  XXXXXXSRVLNCLTGEGEDTRLSASEMKQLIDNILESDIDRDGTINLSEFHVISRS 180
Db    121  GTLNREDLSRLVNCLTGEGEDTRLSASEMKQLIDNILESDIDRDGTINLSEFHVISRS 180
QY     181  PDFASSFKIVL 191
Db     181  PDFASSFKIVL 191
XX
RESULT 2
AAW64199
ID      AAW64199 standard; Protein; 191 AA.
AC      AAW64199;
XX
XX DT 09-NOV-1998 (first entry)
XX DE Human interferon receptor 1 binding protein IR1B1.
XX KW Interferon receptor 1 binding protein; IR1B1; human; tumour;
XX KW cancer; gene therapy; tissue graft; graft survival.
XX OS Homo sapiens.
XX PN WO9831796-A1.
XX PD 23-JUL-1998.
XX PF 15-JAN-1998; 98WO-US00671.
XX PR 15-JAN-1997; 97US-0035636.
XX PA (MCIN/) MCINNIS P A.
XX PA (YEDA ) YEDA RES & DEV CO LTD.
XX PI Abramovitch C, Chebath JE, Revel M;
XX WPI; 1998-414096/35.

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XX PN WO9826056-A1.
XX PD 18-JUN-1998.
XX PF 25-NOV-1997; 97WO-US21603.
XX PR 12-DEC-1996; 96US-0764563.
XX PA (INCY-) INCYTE PHARM INC.
XX PI Goli SK, Hillman JL;
XX DR WPI; 1998-348518/30.
XX DR N-PSDB; V398009.
PT New protein phosphatase regulatory sub-unit - useful for diagnosis,
PT prevention and treatment of immuno-suppression, neuro-degeneration,
PT inflammation and cancer
XX PS Claim 1; Fig 1; 65pp; English.
XX CC The present sequence is a pure human protein phosphatase regulatory
CC subunit (HCNB). Host cells, comprising a vector containing DNA encoding
CC HCNB, are used to produce recombinant HCNB which is used to treat or
CC prevent immunosuppression or neurological diseases (especially parasitic,
CC bacterial or viral infections, including AIDS; the effects of radio- or
CC chemo-therapy and Alzheimer's disease). Antagonists which bind
CC specifically to HCNB and modulate its activity are used to treat
CC inflammation, cancer, or immunological disorders and allograft rejection
CC (especially anaemia, asthma, systemic lupus erythematosus, myasthenia
CC gravis, diabetes, thyroiditis, ulcerative colitis, osteoporosis and
CC arthritis). Complements of the DNA encoding HCNB are useful as probes
CC and primers for detecting the DNA encoding HCNB by hybridisation or
CC amplification assays, while Ab can be used to detect HCNB by immunoassay,
CC particularly for diagnosis of the specified disorders, including early
CC diagnosis of cancers. The probes can also be used to map the
CC corresponding genomic sequence, while Ab are also useful in drug
CC screening and for purifying native HCNB. Therapeutic agents are
CC administered orally, intravenously, intramuscularly, topically or
CC rectally, normally at 0.1-105 mu g.
XX SO Sequence 191 AA;
Query Match 96.8%; Score 875; DB 19; Length 191;
Best Local Similarity 92.1%; Pred. No. 5.1e-79;
Matches 176; Conservative 13; Mismatches 2; Indels 0; Gaps 0;
QY 1 MGGSGSRLSKELLAEOYDITLTKOELLAHRRFCCELLPOEORTVLESSLRAQVFEQILS 60
DB 1 MGGSGSRLSKELLAEOYDITLTKOELLAHRRFCCELLPOEORXXESSLRAQVFEQILS 60
QY 61 LPELKANPFKERICRVFSTSPAKDSLSFEDFLDLVSFSDTATPDIKSHYAFRIFFXXXX 120
DB 61 LPELKANPFKERICRVFSTSPAKDSLSFEDFLDLVSFSDTATPDIKSHYAFRIFFDDDD 120
QY 121 XXXXXXSRVLNCLTGEEDTRLSASEMKQIDNILEESDIDRDGTINLSEFOHVISRS 180
DB 121 GTLNREDLSRLVNCLTGEEDTRLSASEMKQIDNILEESDIDRDGTINLSEFOHVISRS 180
QY 181 PDFASSFKIVL 191
DB 181 PDFASSFKIVL 191
RESULT 4
AAU87324
ID AAU87324 standard; Protein; 172 AA.
XX AC AAU87324;
XX DT 05-JUN-2002 (first entry)
XX

DE Novel central nervous system protein #234.
XX KW Central nervous system; CNS; autoimmune disease; rheumatoid arthritis;
KW hyperproliferative disorder; neoplasm; cardiovascular disorder;
KW cardiac arrest; cerebrovascular disorder; ischaemia; angiogenesis;
KW nervous system disorder; Alzheimer's disease; AIDS; ocular disorder;
KW acquired immunodeficiency virus; dysphagia; gastrointestinal disorder;
KW adenocarcinoma; reproductive system disorder; cancer; testicular feminisation;
KW endocrine disorder; diabetes; cancer; leukaemia; neovascularisation;
KW respiratory disorder; renal disorder; kidney failure; blood disorder;
KW myocardial infarction; wound healing; cell proliferation; skin aging;
KW food additive; food preservative; gene therapy.
XX OS Homo sapiens.
XX PN WO200155318-A2.
XX PD 02-AUG-2001.
XX PF 17-JAN-2001; 2001WO-US01332.
XX PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 14-JUL-2000; 2000US-0217496.
PR 26-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.

XX DE Human polypeptide SEQ ID NO 240.
XX KW Human; antiarthritic; antirheumatic; antiproliferative; vasotropic;
KW cerebroprotective; nootropic; neuroprotective; antibacterial; virucide;
KW fungicide; ophthalmological; cytostatic; immunosuppressive; nootropic;
KW neuroprotective; antiallergic; hepatotropic; antidiabetic;
KW antiinflammatory; antilulcer; vulnery; anticonvulsant; antibacterial;
KW antiparasitic; cardiant; gene therapy; cancer; immune disorder;
KW cardiovascular disorder; neurological disease; infection; human.
XX OS Homo sapiens.
XX PN WO200155308-A2.
XX PD 02-AUG-2001.
XX PF 17-JAN-2001; 2001WO-US01309.
XX PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226868.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.

PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234224.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.

PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
DR WPI; 2001-488781/53.
DR N-PSDB; AAI63868.
XX
PT New isolated nucleic acids and polypeptides, useful for diagnosing,
PT treating and/or preventing human diseases and disorders -
XX
PS Claim 11; SEQ ID NO 240; 664pp + Sequence Listing; English.
XX
CC The invention relates to human polynucleotides (AAI63803-AAI64012) and
CC the encoded proteins (AAM434497-AAM43660) useful for preventing, treating
CC or ameliorating medical conditions e.g. by protein or gene therapy. The
CC genes were isolated from a range of human tissues disclosed in the
CC specification. The nucleic acids, proteins, antibodies and (ant)agonists
CC are useful in the diagnosis, treatment and prevention of: (a) cancer,
CC e.g. breast and ovarian cancer and other cancers of the adrenal gland,
CC bone, bone marrow, breast, gastrointestinal tract, liver, lung, or
CC urogenital; (b) immune disorders e.g. Addison's disease, allergies,
CC autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus,
CC Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative
CC colitis; (c) cardiovascular disorders such as myocardial ischaemias;
CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
CC and parasitic infections.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 184 AA;

Query Match 39.2%; Score 354; DB 22; Length 184;
Best Local Similarity 40.7%; Pred. No. 9.7e-27;
Matches 72; Conservative 44; Mismatches 51; Indels 10; Gaps 3;

QY 13 LAEYQDLTFLTKQEIILAHRRFCELLPQEQRTVSSLRQVFPFEQILSLPELKANPKER 72
Db 13 LEYQALTLTRNEILCIHTDFLKLCPGKYKATL----TMDQVSSLPALRVNPFDR 68

QY 73 ICRVFTSPAKDLSLSEFEDFLDLVSVSDTATPDIKSHYAFRIFFXXXXXXXSRLV 132
Db 69 ICRVFS---HKGMFSEFEDVLGMASVFSEQACPSLKIEYAFRIYDFNENGFIDEEDLQRII 125

QY 133 NCLTGEGETRLSASEMKQLIDNILEESDIDRDGTINLSFEFQHVISRSPDFASFEKI 189
Db 126 LRLNLSDD---MSEDLMLDLTNHVLSESLDNDNMLSFSEFEHAMAKSPDFMNSFRI 179

RESULT 6
AAB64418
ID AAB64418 standard; Protein; 185 AA.
XX
AC AAB64418;
XX
DT 22-MAR-2001 (first entry)
XX
DE Amino acid sequence of human intracellular signalling molecule INTRA50.
XX
KW Human; intracellular signalling molecule; INTRA; immunosuppressive;
KW cytostatic; neuroprotective; nootropic; antiarteriosclerotic; cancer;
KW antiinflammatory; anti-HIV; neuroleptic; antibacterial; antifungal;

KW antiviral; antiparasitic; antihelminthic; antiparkinsonian; AIDS;
KW cell proliferative disorder; arteriosclerosis autoimmune; epilepsy;
KW inflammatory disorder; Addison's disease; gastrointestinal disorder;
KW neurological disorder; Parkinson's disease; Creutzfeldt-Jakob disease;
KW mental disorder; schizophrenia; anxiety.
XX
OS Homo sapiens.
XX
PN WO200077040-A2.
XX
PD 21-DEC-2000.
XX
XX 16-JUN-2000; 2000WO-US16636.
PF
XX
PR 16-JUN-1999; 99US-0139566.
PR 17-AUG-1999; 99US-0149640.
PR 09-NOV-1999; 99US-0164417.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Yue H, Tang YT, Hillman JL, Lal P, Bandman O, Baughn MR;
PI Azimzai Y, Yang J, Reddy R, Lu DAM;
XX
DR WPI; 2001-0253334/03.
DR N-PSDB; AAF32687.
XX
PT New human intracellular signaling molecules, useful for the diagnosis,
PT prevention and treatment of cell proliferative, autoimmune,
PT inflammatory, neurological, gastrointestinal, reproductive and
PT developmental disorders -
XX
PS Claim 5; Page 158-159; 192pp; English.
XX
CC Sequences AAF32638 - AAF32689 represent cDNA encoding human
CC intracellular signalling molecules INTRA1 - INTRA52, represented in
CC AAB64369 - AAB64420. Modulators of the intracellular signalling molecules
CC of the invention exhibit immunosuppressive; cytostatic; neuroprotective;
CC nootropic; antiarteriosclerotic; antiinflammatory; anti-HIV;
CC neuroleptic; antibacterial; antifungal; antiviral; antiparasitic;
CC antihelminthic; and antiparkinsonian activity. INTRA polypeptides their
CC agonists and antagonists are useful for the treatment of a condition
CC associated with decreased or increased expression of functional INTRA.
CC Disorders associated with abnormal INTRA expression or activity include
CC cell proliferative disorders e.g. arteriosclerosis and cancers;
CC autoimmune or inflammatory disorders e.g. Addison's disease and acquired
CC immunodeficiency syndrome (AIDS); viral, bacterial, fungal, parasitic,
CC protozoal and helminthic infections; gastrointestinal disorders e.g.
CC dysphagia and irritable bowel syndrome; neurological disorders e.g.
CC epilepsy and Parkinson's disease; prion diseases e.g. Creutzfeldt-Jakob
CC disease and mental disorders e.g. anxiety, schizophrenia and Tourette's
CC disorder. Antibodies immuno specific for the INTRA proteins may also be
CC useful in the diagnosis of the above disorders.
XX
SQ Sequence 185 AA;

Query Match 38.9%; Score 352; DB 22; Length 185;
Best Local Similarity 40.8%; Pred. No. 1.5e-26;
Matches 73; Conservative 43; Mismatches 53; Indels 10; Gaps 3;

QY 11 ELLAEYQDLTFLTKQEIILAHRRFCELLPQEQRTVSSLRQVFPFEQILSLPELKANPK 70
Db 12 EDLEEQALTLTRNEILCIHTDFLKLCPGKYKATL----TMDQVSSLPALRVNPF 67

QY 71 ERICRVFTSPAKDLSLSEFEDFLDLVSVSDTATPDIKSHYAFRIFFXXXXXXXSR 130
Db 68 DRICRVFS---HKGMFSEFEDVLGMASVFSEQACPSLKIEYAFRIYDFNENGFIDEEDLQ 124

QY 131 LVNCLTGEGETRLSASEMKQLIDNILEESDIDRDGTINLSFEFQHVISRSPDFASFEKI 189
Db 125 IILRLNLSDD---MSEDLMLDLTNHVLSESLDNDNMLSFSEFEHAMAKSPDFMYSFRI 180

RESULT 7

KW	myocardial infarction; wound healing; cell proliferation; skin aging;
KW	food additive; food preservative; gene therapy.
XX	
OS	Homo sapiens.
PN	WO200155318-A2.
XX	
PD	02-AUG-2001.
XX	
PF	17-JAN-2001; 2001WO-US01332.
XX	
PR	31-JAN-2000; 2000US-0179065.
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PR	11-DEC-2000;	2000US-0254097.
PR	05-JAN-2001;	2001US-0259678.
XX		
PA	(HUMA-) HUMAN GENOME SCI INC.	
XX		
PI	Rosen CA,	Barash SC, Ruben SM;
XX		
DR	WPI; 2001-465570/50.	

```

DR N-PSDB; AAL01332.
XX
XX Isolated nucleic acid molecule encoding a reproductive system antigen
PT is used in preventing, treating or ameliorating a medical condition -
XX
XX Claim 11; SEQ ID NO 4020; 1297bp + Sequence Listing; English.
PS
XX The present invention provides the protein and coding sequences of a
CC number of human reproductive system related antigens. These can be used
CC in the prevention and treatment of reproductive system disorders,
CC including cancer. The present sequence is a protein of the invention.
XX
SQ Sequence 173 AA;

Query Match          36.3%; Score 328; DB 22; Length 173;
Best Local Similarity 39.48; Pred. No. 3.5e-24;
Matches 69; Conservative 43; Mismatches 53; Indels 10; Gaps 3;

QY 13 LAEYQDLFLTKQEILLAHRRFCCELLPQEQRTVESSLRAQVPFEQILSLPELKANPFKER 72
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Db 1 LEEYQALTFLTRNEILCIHDTFLKICPPGKYKEATL---TMDQVSSLPALRVNPERDR 56

QY 73 ICRVFSTSPAKDLSFEDFDLLSVESDTPDPDIKSHYAFRIFXXXXXXXSRVL 132
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QY 133 NCLTGEGEDTRLASASEMKQLIDNILESDIDRDGTINTLSEFGHYISRSPDFASSF 187
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Db 114 LRLLNSDD---MSEDLLMDLTNVHLXSXSDLNDNMLSFSEFEHAMAKSPDFMTPE 165

RESULT 11
AAM43637
ID AAM43637 standard; Protein; 173 AA.
XX
XX AAM43637;
XX
XX 22-OCT-2001 (first entry)
DE Human polypeptide SEQ ID NO 315.
XX
XX Human: antiarthritic; antirheumatic; antiproliferative; vasotropic;
KW cerebroprotective; nootropic; neurotropic; neuroprotective; antiviral; virucide;
KW fungicide; ophthalmological; cytostatic; immunosuppressive; nootropic;
KW neuroprotective; antifungal; hepatotrophic; antidiabetic;
KW antiinflammatory; antitumor; vulnary; anticonvulsant; antibacterial;
KW antiparasitic; cardiant; gene therapy; cancer; immune disorder;
KW cardiovascular disorder; neurological disease; infection; human.
XX
OS Homo sapiens.
XX
XX WO200155308-A2.
PN
XX 02-AUG-2001.
PD
XX 17-JAN-2001; 2001WO-US01309.
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XX 31-JAN-2000; 2000US-0179065.
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PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.

(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Barash SC, Ruben SM;

WPI; 2001-488781/53.

N-PSDB; AAI63943.

New isolated nucleic acids and polypeptides, useful for diagnosing, treating and/or preventing human diseases and disorders -

Claim 11; SEQ ID NO 315; 664pp + Sequence Listing; English.

The invention relates to human polynucleotides (AAI63803-AAI64012) and the encoded proteins (AAM43449/-AAM43660) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes were isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and

Db 43 KDCFTFTKREILRVHKKRFLRPLVPRMTEGQASSVKVPCCECIEMPELR----- 94
QY 74 CRVFSTSPAKDSLSFEDFLDLVSFSDTATPDIKSHYAFRIFFXXXXXXXSRLVN 133
Db 95 -EAFSRD-GQGNLSFEDFLDALSVFSEQAPRDIKVFYAFKIYDFDQDFIGHAD--LMS 149
QY 134 CLTGEEDTRLASSEMOLINDNILEESDIDRDGTINLSEFQHVISRSPDFASSFKI 189
Db 150 CLTFTMTKN-ELSPHEHQIADKVIIEADYDGDGKLSILEFEHVILRAPDFLSTFHI 204
RESULT 14
ABP41194
ID ABP41194 standard; Protein; 169 AA.
XX ABP41194;
AC ABP41194;
XX
DT 23-AUG-2002 (first entry)
XX
DE Human ovarian antigen HTLHN94, SEQ ID NO:2326.
XX
KW Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
KW ovarian cancer; breast cancer; reproductive system disorder;
KW infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
KW PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection;
KW inflammatory condition; immune disorder; blood disorder;
KW cardiovascular disorder; respiratory disorder; neurological disorder;
KW gastrointestinal disorder; urinary system disorder; drug screening;
KW gene therapy; chromosome mapping; forensic analysis;
KW antibody preparation; cytostatic; immunomodulatory; neuroprotective;
KW antiinflammatory; gynaecological; reproductive.
XX
OS Homo sapiens.
XX
PN WO200200677-A1.
XX
PD 03-JAN-2002.
XX
PE 07-JUN-2001; 2001WO-US18569.
XX
PR 07-JUN-2000; 2000US-209467P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Birse CE, Rosen CA;
XX
DR WPI; 2002-147878/19.
DR N-PSDB; ABQ54271.
XX
PT Isolated nucleic acid molecules encoding novel ovarian polypeptides,
PT useful in the prevention, treatment and diagnosis of cancer (e.g.
PT ovarian cancer), immune disorders, cardiovascular disorders and
PT neurological diseases -
XX
PS Claim 11; SEQ ID No 2326; 2922pp; English.
XX
CC The invention relates to 2175 novel human ovarian antigens (ABP41054-
CC ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also
CC encompasses polypeptides 90% identical and polynucleotides 95% identical
CC to the sequences of the invention. The invention additionally relates to
CC recombinant vectors and host cells comprising human ovarian antigen
CC polynucleotides, antibodies against human ovarian antigens, and the use
CC of ovarian antigen polynucleotides and polypeptides in diagnosing,
CC treating, prognosing or preventing various ovarian cancer and breast-related
CC disorders. Such conditions include ovarian cancer and breast cancer, and
CC metastatic tumours of ovarian or breast origin, reproductive system
CC disorders (e.g., infertility, disorders of pregnancy, anovulation,
CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine
CC disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic
CC shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and
CC vaginitis), immune disorders (e.g., congenital and acquired
CC immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),

CC blood-related disorders (e.g., anaemia), cardiovascular disorders,
CC respiratory disorders, neurological disorders, gastrointestinal disorders
CC and urinary system disorders. Ovarian antigen polypeptides and
CC polynucleotides may also be used in screening for compounds which
CC modulate ovarian antigen expression or activity. The polynucleotides may
CC further be used for gene therapy, chromosome mapping, in the
CC identification of individuals and in forensic analysis, and the
CC polypeptides may be used as food additives or to prepare antibodies
CC useful in disease diagnosis, drug targeting and phenotyping. The present
CC sequence represents a human ovarian antigen of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 169 AA;
Query Match 24.9%; Score 225.5; DB 23; Length 169;
Best Local Similarity 33.3%; Pred. No.6.5e-14;
Matches 42; Conservative 44; Mismatches 35; Indels 5; Gaps 2;
QY 64 LKANPFKERICRVFSTSPAKDSLSFEDFLDLVSFSDTATPDIKSHYAFRIFFXXXXXX 123
Db 47 LOENPFKERIYAFAFS-EDGEGNLTFNDFVMSVLCESAPRELKANYAFKIYDFNTDNFI 105
QY 124 XXXXSRLVNCITGEGEDTRLASSEMOLINDNILEESDIDRDGTINLSEFQHVISRSPDF 183
Db 106 CKEDLELTARLT---KSELDDEEVVLVCVKVIEADLDGDGKLGFAFEDMIAPDF 161
QY 184 ASSFKI 189
Db 162 LSTFHI 167
RESULT 15
AAV11976
ID AAV11976 standard; Protein; 120 AA.
XX
AC AAV11976;
XX
DT 18-JUN-1999 (first entry)
XX
DE Human 5' EST secreted protein SEQ ID No: 576.
XX
KW Human; secreted protein; EST; expressed sequence tag; diagnosis;
KW forensic; gene therapy; chromosome mapping; signal peptide; prostate;
KW upstream regulatory sequence; cytokine activity; cell proliferation;
KW differentiation; haematopoiesis regulation; tissue growth regulation;
KW reproductive hormone regulation; chemotactic; chemokinetic; haemostatic;
KW thrombolytic; anti-inflammatory; tumour inhibition.
XX
OS Homo sapiens.
XX
PN WO9906550-A2.
XX
PD 11-FEB-1999.
XX
PE 31-JUL-1998; 98WO-IB01232.
XX
PR 01-AUG-1997; 97US-0905144.
XX
PA (GEST) GENSET.
XX
PI Duclert A, Dumas Milne Edwards J, Lacroix B;
XX
DR WPI; 1999-153780/13.
DR N-PSDB; AAX40698.
XX
PT New isolated prostate-derived nucleic acids - used to develop
PT products which may have cytokine, immune regulatory, haematopoiesis
PT regulating, anti-inflammatory or tumour inhibition activity
XX
PS Claim 34; Page 664; 675pp; English.
XX

Search completed: January 17, 2003, 12:50:57
Job time : 36 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 17, 2003, 12:50:20 ; Search time 15 Seconds
(without alignments)
374.652 Million cell updates/sec

Title: US-09-878-454A-2X
Perfect score: 904
Sequence: 1 MGGSGSRLSKELLAEXQDLT.....EFQHVISRSPDFASSFKIVL 191

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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2: /cgn2_6/ptodata/1/laa/5B.COMB.pep:*
3: /cgn2_6/ptodata/1/laa/6A.COMB.pep:*
4: /cgn2_6/ptodata/1/laa/6B.COMB.pep:*
5: /cgn2_6/ptodata/1/laa/PCTUS.COMB.pep:*
6: /cgn2_6/ptodata/1/laa/Backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	900	99.6	191	4	US-08-720-625-2
2	875	96.8	191	3	US-08-764-563-1
3	201.5	22.3	177	3	US-08-764-563-3
4	189.5	21.0	174	1	US-08-328-322-17
5	178.5	19.7	157	1	US-08-328-322-15
6	171.5	19.0	169	4	US-08-720-625-4
7	171.5	19.0	170	3	US-08-764-563-5
8	155.5	17.2	179	3	US-08-764-563-4
9	151	16.7	186	3	US-08-655-352-8
10	151	16.7	186	4	US-09-258-016-8
11	151	16.7	186	4	US-09-257-825B-8
12	135	14.9	193	3	US-08-655-352-3
13	135	14.9	193	4	US-09-258-016-3
14	135	14.9	193	4	US-09-257-825B-3
15	133.5	14.8	196	3	US-09-048-889-1
16	126	13.9	220	4	US-09-399-913-26
17	126	13.9	220	4	US-09-298-731-26
18	125	13.8	191	3	US-08-655-352-7
19	125	13.8	191	4	US-09-258-016-7
20	125	13.8	191	4	US-09-257-825B-7
21	123	13.6	193	3	US-08-655-352-4
22	123	13.6	193	4	US-09-258-016-4
23	123	13.6	193	4	US-09-257-825B-4
24	121	13.4	220	4	US-09-399-913-24
25	121	13.4	220	4	US-09-298-731-24
26	121	13.4	252	4	US-09-399-913-20
27	121	13.4	252	4	US-09-298-731-20

28	121	13.4	270	4	US-09-399-913-14	Sequence 14, Appl
29	121	13.4	270	4	US-09-298-731-14	Sequence 14, Appl
30	119.5	13.2	172	4	US-09-285-601-2	Sequence 2, Appl1
31	119	13.2	193	3	US-08-655-352-2	Sequence 2, Appl1
32	119	13.2	193	4	US-09-258-016-2	Sequence 2, Appl1
33	118	13.1	193	4	US-09-257-825B-2	Sequence 2, Appl1
34	118	13.1	270	4	US-09-399-913-18	Sequence 18, Appl
35	118	13.1	270	4	US-09-298-731-18	Sequence 18, Appl
36	116	12.8	216	4	US-09-399-913-6	Sequence 6, Appl1
37	116	12.8	216	4	US-09-298-731-6	Sequence 6, Appl1
38	116	12.8	225	4	US-09-399-913-30	Sequence 30, Appl
39	116	12.8	225	4	US-09-298-731-30	Sequence 30, Appl
40	116	12.8	227	4	US-09-399-913-8	Sequence 8, Appl1
41	116	12.8	227	4	US-09-399-913-10	Sequence 10, Appl
42	116	12.8	227	4	US-09-298-731-8	Sequence 8, Appl1
43	116	12.8	227	4	US-09-298-731-10	Sequence 10, Appl
44	116	12.8	245	4	US-09-399-913-4	Sequence 4, Appl1
45	116	12.8	245	4	US-09-298-731-4	Sequence 4, Appl1

ALIGNMENTS

RESULT 1
US-08-720-625-2
; Sequence 2, Application US/08720625
; Patent No. 6242587
; GENERAL INFORMATION:
; APPLICANT: Nalk, Ulhas P.
; APPLICANT: Parise, Leslie V.
; TITLE OF INVENTION: CALCIUM-INTEGRIN BINDING PROTEIN
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESS: Bell, Seltzer, Park & Gibson
; STREET: P.O. Drawer 34009
; CITY: Charlotte
; STATE: No. 6242587th Carolina
; COUNTRY: USA
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/720,625
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sibley, Kenneth D.
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 5470-138
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-420-2200
; TELEFAX: 919-881-3175
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 191 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-720-625-2

Query Match 99.6%; Score 900; DB 4; Length 191;
Best Local Similarity 92.7%; Pred. No. 1.1e-92;
Matches 177; Conservative 14; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGGSGSRLSKELLAEXQDLTFLTKQETLLAHRFCCELLPQEQRTVESSLRQVPEQILS 60
|||||
Db 1 MGGSGSRLSKELLAEXQDLTFLTKQETLLAHRFCCELLPQEQRTVESSLRQVPEQILS 60
|||||
QY 61 LPELKNPFKERICRVFSTSPAKDSLSPEDFLDLLSVFSDTATPDIKSHYAFRIFFXXXXX 120
|||||

Db 61 LPELKANPFKERICRVFSTSPAKDSLSFEDFLDLLSVFSDTATPDIKSHYAFRIFEDDDD 120

QY 121 XXXXXXXXSRVLNCLTGEGETRLSASEMKQLIDNILEESDIDRDGTINLSEFQHVISR 180

Db 121 GTLNREDLSRLVNLCTGEGETRLSASEMKQLIDNILEESDIDRDGTINLSEFQHVISR 180

QY 181 PDFASSEFKIVL 191

Db 181 PDFASSEFKIVL 191

RESULT 2

US-08-764-563-1

; Sequence 1, Application US/08764563

; Patent No. 6093565

; GENERAL INFORMATION:

; APPLICANT: Hillman, Jennifer L.

; APPLICANT: Goli, Surya K.

; TITLE OF INVENTION: A NOVEL PROTEIN PHOSPHATASE

; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Incyte Pharmaceuticals, Inc.

; STREET: 3174 Porter Drive

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/764,563

; FILING DATE: Herewith

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Billings, Lucy J.

; REGISTRATION NUMBER: 36,749

; REFERENCE/DOCKET NUMBER: PF-0178 US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-855-0555

; TELEFAX: 415-845-4166

; TELEX:

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 191 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; IMMEDIATE SOURCE:

; LIBRARY: Consensus

; CLONE: Consensus

US-08-764-563-1

Query Match 96.8%; Score 875; DB 3; Length 191;

Best Local Similarity 92.1%; Pred. No. 7e-90;

Matches 176; Conservative 13; Mismatches 2; Indels 0; Gaps 0;

QY 1 MGGSGSRLSKELLAEQDLTFLTKQEILLAHRRFCELLPQEQRTVLESSLRAQVPFEQILS 60

Db 1 MGGSGSRLSKELLAEQDLTFLTKQEILLAHRRFCELLPQEQRXESSLRAQVPFEQILS 60

QY 61 LPELKANPFKERICRVFSTSPAKDSLSFEDFLDLLSVFSDTATPDIKSHYAFRIFXXXXX 120

Db 61 LPELKANPFKERICRVFSTSPAKDSLSFEDFLDLLSVFSDTATPDIKSHYAFRIFDFFDD 120

QY 121 XXXXXXXXSRVLNCLTGEGETRLSASEMKQLIDNILEESDIDRDGTINLSEFQHVISR 180

Db 121 GTLNREDLSRLVNLCTGEGETRLSASEMKQLIDNILEESDIDRDGTINLSEFQHVISR 180

QY 181 PDFASSEFKIVL 191

Db 181 PDFASSEFKIVL 191

RESULT 3

US-08-764-563-3

; Sequence 3, Application US/08764563

; Patent No. 6093565

; GENERAL INFORMATION:

; APPLICANT: Hillman, Jennifer L.

; APPLICANT: Goli, Surya K.

; TITLE OF INVENTION: A NOVEL PROTEIN PHOSPHATASE

; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Incyte Pharmaceuticals, Inc.

; STREET: 3174 Porter Drive

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/764,563

; FILING DATE: Herewith

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Billings, Lucy J.

; REGISTRATION NUMBER: 36,749

; REFERENCE/DOCKET NUMBER: PF-0178 US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-855-0555

; TELEFAX: 415-845-4166

; TELEX:

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 177 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; IMMEDIATE SOURCE:

; LIBRARY: GenBank

; CLONE: 458230

US-08-764-563-3

Query Match 22.3%; Score 201.5; DB 3; Length 177;

Best Local Similarity 26.4%; Pred. No. 4.4e-14;

Matches 47; Conservative 50; Mismatches 68; Indels 13; Gaps 3;

QY 1 MGGSGSRLSKELLAEQDLTFLTKQEILLAHRRFCELLPQEQRTVLESSLRAQVPFEQILS 60

Db 1 MGTNTSLRPEEVEEMQGTNFTQKEIKLYKRFKKLDKDGNGTISK-----DEFLM 52

QY 61 LPELKANPFKERICRVFSTSPAKDSLSFEDFLDLLSVFSDTATPDIKSHYAFRIFXXXXX 120

Db 53 IPELAVNPLVKRVISIFDEN-GDGSVNFKEIFAALSVFNAQGDQKQKLEFAFKVYDIDGD 111

QY 121 XXXXXXXXSRVLNCLTGEGETRLSASEMKQLIDNILEESDIDRDGTINLSEFQHVIS 178

Db 112 GYISNGELFTVLKMMVG---NNLSDVQLQIIVDKTILEADEDGDGKISFEFAKTLS 165

RESULT 4

US-08-328-322-17

; Sequence 17, Application US/08328322

```

: Patent No.5723436
: GENERAL INFORMATION:
: APPLICANT: Huang, Laiqiang
: APPLICANT: Cyert, Martha S.
: TITLE OF INVENTION: Calcineurin Interacting Protein Compositions
: TITLE OF INVENTION: and Methods
: NUMBER OF SEQUENCES: 23
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Dehlinger & Associates
: STREET: 350 Cambridge Avenue, Suite 250
: CITY: Palo Alto
: STATE: CA
: COUNTRY: USA
: ZIP: 94306
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/328,322
: FILING DATE: 24-OCT-1994
: CLASSIFICATION: 530
: ATTORNEY/AGENT INFORMATION:
: NAME: Sholtz, Charles K.
: REGISTRATION NUMBER: P38,615
: REFERENCE/DOCKET NUMBER: 8600-0151.10
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 324-0880
: TELEFAX: (415) 324-0960
: INFORMATION FOR SEQ ID NO: 17:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 174 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
US-08-328-322-17

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Query Match	21.0%	Score 189.5;	DB 1;	Length 174;
Best Local Similarity	24.3%	Pred. No. 9.5e-13;		
Matches 43;	Conservative 54;	Mismatches 63;	Indels 17;	Gaps 4;

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Db      49 IPGVSSNPPLAGRIMEVFADANSGD-VDFQEFTLGSLIFSGRGSKEKLRFAFKIYDIDKD    107

QY      121 XXXXXXXXXSRLVNCLTGEGEDTRLASASEMKOLIDNILESDIDRDGTINLSEFOHVI    177
        : : : : : : : : | : : : : : : : : : : : : : : : : : : : : : : :
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RESULT 5
 US-08-328-322-15
 ; Sequence 15, Application US/08328322
 ; Patent No. 5723436
 ;
 ; GENERAL INFORMATION:
 ; APPLICANT: Huang, Laiqiang
 ; APPLICANT: Cyert, Martha S.
 ; TITLE OF INVENTION: Calcineurin Interacting Protein Compositions
 ; TITLE OF INVENTION: and Methods
 ; NUMBER OF SEQUENCES: 23
 ;
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Dehlinger & Associates
 ; STREET: 350 Cambridge Avenue, Suite 250
 ; CITY: Palo Alto
 ; STATE: CA
 ;
 ; COUNTRY: USA
 ; ZIP: 94306
 ;
 ; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/328,322
; FILING DATE: 24-OCT-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Sholtz, Charles K.
; REGISTRATION NUMBER: P38,615
; REFERENCE/DOCKET NUMBER: 8600-0151.10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEO ID NO: 15;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 157 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-322-15

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Query Match	19.7%;	Score 178.5;	DB 1;	Length 157;
Best Local Similarity	24.0%;	pred. No. 1.3e-11;		
Matches	37;	Conservative	50;	Mismatches 54;
			Indels	13;
			Gaps	3;

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OY      24 KOEILLAHRECELLPOEQRTVSSLRACVPFEQILSLPELKANPFKERICRVFSTSPAK   83  
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Db       3 RDEIERLKRKRMKLDRDSSGSDKN-----EFMSIPGVSNPLAGRIMEVFADANS    54  
  
OY      84 DLSLFEDFLDLVSFSDDTATPDIKSHVAFRIFXXXXXXXSRVLVNCLTGEGEDTR   143  
        .| : | : | : | : | : | : | : | : | : | :  
Db       55 D-VDFQEFTIGSIFSGRSGSKDEKRLRAFKIYIDDKDGFI SNGELEIVLKIMVG----SN 109  
  
OY     144 LSASEMKQLDNILLEESDIDRDGTINLSEFHVI   177  
        - : : : : | : | : | : | : | : | : | :  
Db     110 LDDEGLQIQYDRVENDSDGDGRLSFEFFKNAI   143
```

RESULT

US-08-720-625-4
: Sequence 4, Application US/08720625
: Patent No. 6242587
: GENERAL INFORMATION:
: APPLICANT: Naik, vihas P.
: APPLICANT: Parise, Leslie V.
: TITLE OF INVENTION: CALCIUM-INTEGRIN BINDING PROTEIN
: NUMBER OF SEQUENCES: 10
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Bell, Seltzer, Park & Gibson
: STREET: P.O. Drawer 34009
: CITY: Charlotte
: STATE: No. 6242587th Carolina
: COUNTRY: USA
: ZIP: 28234
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/720,625
: FILING DATE:
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Sibley, Kenneth D.
: REGISTRATION NUMBER: 31,665
: REFERENCE/DOCKET NUMBER: 5470-138
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 919-420-2200
: TELEFAX: 919-881-3175
: INFORMATION FOR SEQ ID NO: 4:


```

; SEQUENCE CHARACTERISTICS:
; LENGTH: 169 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-720-625-4

Query Match
Best Local Similarity 19.0%; Score 171.5; DB 4; Length 169;
Matches 33; Conservative 42; Mismatches 42; Indels 5; Gaps 2;

QY 56 EQILSLPELKANPKERICRVFSTSPAKDLSFEDFLDLLSVFSDTATPDIKSHYAFRIF 115
|: :||||: || :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|:
Db 40 EEFMSLPQLQNPLVQRVIDIFDTD-GNGEVDKFEFIEGVSVKGDKEQKLRFAFRIY 98

QY 116 XXXXXXXXXXXXXSRVLNCLTGEGETRLSASEMKQLIDNILEESDIDRDGTINLSEFQH 175
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 99 DMDKDGYSINGELFQVLKMMVG----NNLKDTQLQIQIVDKTIINADKDGGRISFEFCA 154

QY 176 VI 177
|:
Db 155 VV 156

RESULT 7
US-08-764-563-5
; Sequence 5, Application US/08764563
; Patent No. 6093565
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: A NOVEL PROTEIN PHOSPHATASE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION NUMBER: US/08/764,563
; APPLICATION NUMBER: 36,749
; FILING DATE: Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0178 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 170 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 461682
US-08-764-563-5

Query Match
19.0%; Score 171.5; DB 3; Length 170;
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Best Local Similarity 27.0%; Pred. No. 9.7e-11;
Matches 33; Conservative 42; Mismatches 42; Indels 5; Gaps 2;

QY 56 EQILSLPELKANPKERICRVFSTSPAKDLSFEDFLDLLSVFSDTATPDIKSHYAFRIF 115
|: :||||: || :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|:
Db 41 EEFMSLPQLQNPLVQRVIDIFDTD-GNGEVDKFEFIEGVSVKGDKEQKLRFAFRIY 99

QY 116 XXXXXXXXXXXXXSRVLNCLTGEGETRLSASEMKQLIDNILEESDIDRDGTINLSEFQH 175
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 100 DMDKDGYSINGELFQVLKMMVG----NNLKDTQLQIQIVDKTIINADKDGGRISFEFCA 155

QY 176 VI 177
|:
Db 156 VV 157

RESULT 8
US-08-764-563-4
; Sequence 4, Application US/08764563
; Patent No. 6093565
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: A NOVEL PROTEIN PHOSPHATASE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/764,563
; FILING DATE: Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0178 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 179 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 109612
US-08-764-563-4

Query Match
17.2%; Score 155.5; DB 3; Length 179;
Best Local Similarity 24.5%; Pred. No. 6.9e-09;
Matches 37; Conservative 39; Mismatches 62; Indels 13; Gaps 3;

QY 35 CELLPQEQ-----RTVESSLRAQVPFEQILSLPELKANPKERICRVFSTSPAKDSL 86
| :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|:
Db 12 CNHFDQEEIRRLGKSFRLDLDDKSGSLSEEFMRLPELQNPVGRVIDIFDTD-GNGEV 70

QY 87 SFEDFLDLLSVFSDTATPDIKSHYAFRIFXXXXXXXXXXXXXXXXXXXXXXXXXXXX 146
| :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|:
;
```

Db 71 DFHEFIVGTSQFSVKGDEEQKLRFAFRIDMDNDGFISNGELFQVLMKMGV---NNLKD 126
QY 147 SEMKOLIDNILESDDIRDTGINSFQHV 177
Db 127 WOLQOLVKSILVLDKDGGRISFEESDV 157

RESULT 9
US-08-655-352-8

; Sequence 8, Application US/08655352
; Patent No. 6077991
; GENERAL INFORMATION:
; APPLICANT: Bachettira W. Poovaiyah, Zhilua Liu,
; APPLICANT: Shameekumar Patil, Datsuke Takezawa
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: PRODUCTION OF MALE-STERILE PLANTS
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klarquist Sparkman Campbell Leigh &
; ADDRESSEE: Winston, LLP
; STREET: One World Trade Center
; STREET: 121 S.W. Salmon Street
; STREET: Suite 1600
; CITY: Portland
; STATE: Oregon
; COUNTRY: United States of America
; ZIP: 97204
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Disk, 3-1/2 inch
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/655,352
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/323,449
; FILING DATE: October 14, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Dow, Alan. E.
; REGISTRATION NUMBER: 35,123
; REFERENCE/DOCKET NUMBER: 4630-45000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (503) 226-7391
; TELEFAX: (503) 228-9446
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 186 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; DESCRIPTION: Region of Drosophila frequen in
; DESCRIPTION: (Gen2:Drofreg) with homology to 111y
; DESCRIPTION: CcAMK
; US-08-655-352-8

Query Match 16.7%; Score 151; DB 3; Length 186;
Best Local Similarity 22.3%; Pred. No. 2.4e-08;
Matches 44; Conservative 49; Mismatches 82; Indels 22; Gaps 5;
QY 1 MGGSGSRLSKELLAEYQDLTLTKQELLAHRRFCELLPQEQRTVESSLRAQVPFEQILS 60
Db 1 MGKSSSKLKQDITDLTLTDYTFTEKEIRQWHKGFLLKDCPNGLLTEQGFIRIKYQF----- 55
QY 61 LPELKANPEKERICRVFSTSPAKDSLFEDFLDLVSFSDTATPDIKSHYAFRIFFXXXXX 120
Db 56 FPQGDPSKFAFLVRFVDEN-NDGSIFFEFIRALSVTSKGL--DEKIQWAFRLYDVND 112
QY 121 XXXXXXXXSRVNL-----TGEGETRLSASEMKOLIDNILESDDIRDTGINTLSE 172
Db 113 GYITREMYNIYDAIYQMGVGOQPOSEDENT-----PQKRVDKIFDQMDKNHDKLTLEE 166

QY 173 FOHVISRSPDFASSFKI 189
Db 167 FREGSKADPRIVQALSL 183

RESULT 10

US-09-258-016-8
; Sequence 8, Application US/09258016
; Patent No. 6362395
; GENERAL INFORMATION:
; APPLICANT: Bachettira W. Poovaiyah, Zhilua Liu,
; APPLICANT: Shameekumar Patil, Datsuke Takezawa
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: PRODUCTION OF MALE-STERILE PLANTS
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klarquist Sparkman Campbell Leigh &
; ADDRESSEE: Winston, LLP
; STREET: One World Trade Center
; STREET: 121 S.W. Salmon Street
; STREET: Suite 1600
; CITY: Portland
; STATE: Oregon
; COUNTRY: United States of America
; ZIP: 97204
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Disk, 3-1/2 inch
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/258,016
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Stephens Jr., Donald L.
; REGISTRATION NUMBER: 34,022
; REFERENCE/DOCKET NUMBER: 4630-51994
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (503) 226-7391
; TELEFAX: (503) 228-9446
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 186 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; DESCRIPTION: Region of Drosophila frequen in
; DESCRIPTION: (Gen2:Drofreg) with homology to 111y
; DESCRIPTION: CcAMK
; US-09-258-016-8

Query Match 16.7%; Score 151; DB 4; Length 186;
Best Local Similarity 22.3%; Pred. No. 2.4e-08;
Matches 44; Conservative 49; Mismatches 82; Indels 22; Gaps 5;
QY 1 MGGSGSRLSKELLAEYQDLTLTKQELLAHRRFCELLPQEQRTVESSLRAQVPFEQILS 60
Db 1 MGKSSSKLKQDITDLTLTDYTFTEKEIRQWHKGFLLKDCPNGLLTEQGFIRIKYQF----- 55
QY 61 LPELKANPEKERICRVFSTSPAKDSLFEDFLDLVSFSDTATPDIKSHYAFRIFFXXXXX 120
Db 56 FPQGDPSKFAFLVRFVDEN-NDGSIFFEFIRALSVTSKGL--DEKIQWAFRLYDVND 112
QY 121 XXXXXXXXSRVNL-----TGEGETRLSASEMKOLIDNILESDDIRDTGINTLSE 172
Db 113 GYITREMYNIYDAIYQMGVGOQPOSEDENT-----PQKRVDKIFDQMDKNHDKLTLEE 166
QY 173 FOHVISRSPDFASSFKI 189
Db 167 FREGSKADPRIVQALSL 183


```

1 NAME: Stephens Jr., Donald L.
2 REGISTRATION NUMBER: 34,022
3 REFERENCE/DOCKET NUMBER: 4630-51994
4 TELECOMMUNICATION INFORMATION:
5 TELEPHONE: (503) 226-7391
6 TELEFAX: (503) 228-9446
7 INFORMATION FOR SEQ ID NO: 3:
8 SEQUENCE CHARACTERISTICS:
9 LENGTH: 193 amino acids
10 TYPE: amino acid
11 TOPOLOGY: 1linear
12 MOLECULE TYPE: protein
13 DESCRIPTION: Region of rat neural visinin-like protein
14 DESCRIPTION: (Gen2:Ratnvp3) with homology to 1lly
15 DESCRIPTION: CCamk
16
17 US-09-258-016-3

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Query Match	14.98;	Score 135;	DB 4;	Length 193;
Best Local Similarity	22.68;	Pred. No. 1.6e-06;		
Matches 47; Conservative	50;	Mismatches 75;	Indels 36;	Gaps 7;

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QY      1 MGGSGSRLSKELLAEYODTLFTLKQEIILAHRRFCELLPQEQRVSSLRAQVPFEQILS    60
        ||  |::|:|:|:|  ||  ::|:|  ||:|  |:|:|
Db      1 MGKQNSKLRPVELQDLREHTEFTDHELOEWYKGFLKDPCPTGHLTYDE-----FKKIYA  53
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QY      61  --LPELKANPFKERICRVFSTSPAKDSLSFEDFLDLSVFSDTATPDIKSHYAFRIFXXX 118
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db      54  NFFPYGDASKFAEHVFRFTDIN-SDGTIDREFRFIIALSVTS-RGKLEQIKMAFSMYDLD 111

```

```

Qy 119 XXXXXXXXXXXXSLVNCITGEGEDTRLSASEMK-----QLIDNILESDIDRDGTIN 169
      ::::: ::: ::: ::: ::: ::: ::: ::: ::: ::: :::
Db 112 GNGYISRSEMLEIVQAI-----YKMVSSVMKMPEDESTPEKRTDKIFRGMDINNDGKLS 165

```

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OY 170 LSEF-----QHVISRSPDEASSF 187
    1 1 1 : 1 1 1
Db 166 LEEFIKGAKSDPSIVRLQCDPSSASQF 193

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RESULT 14
US-09-257-825B-3
Sequence 3, Application US/09257825B

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GENERAL INFORMATION:
APPLICANT: Poovalah, Bachettlira W.
APPLICANT: Patil, Shameekumar
APPLICANT: Takezawa, Daisuke
TITLE OF INVENTION: Compositions and Methods for Production of Male-Sterile Plants
FILE REFERENCE: 4630-51993
CURRENT APPLICATION NUMBER: US/09/257,825B
CURRENT FILING DATE: 1999-02-25
PRIOR APPLICATION NUMBER: US 08/655,352
PRIOR FILING DATE: 1996-05-23
PRIOR APPLICATION NUMBER: US 60/014,743
PRIOR FILING DATE: 1996-03-28
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 193
TYPE: PRT
ORGANISM: Rat
US-09-257-825B-3

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Query Match	14.9%;	Score 135;	DB 4;	length 193;
Best Local Similarity	22.6%;	Pred. No. 1.6e-06;		
Matches 47;	Conservative 50;	Mismatches 75;	Indels 36;	Gaps 7;

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QY      1 MGGSGSRSLKELLAEYODLTFTLKOEILLAHRRFCCELLPQEORTVESLSRAQVPFEQILS   60
        ||    || : | : : | | : : : | : : : | : : : | : : : | : : : | : : :
Db      1 MGKONSRLRPEVLQDLREHTEFTHDELOEWTKGFLKDCCPTGHLLTVDE-----FKKIYA   53
```

QY 61 --LPFLKANPEKERICRVSTSPAKDSLSEFEDFLDLLSVSDTATPDIKSHYAFRIFXXX 118
 | : | : | :
Db 54 NFFPYGDASKFAEHVERFTDIN-SDGTIDFREFIILSVTS-RGKLEOKIKWAFSMYDLD 111

```

QY 119 XXXXXXXXXXXXSRVNCLTGEGEDTRLASAMK-----QLIDNILEESDIDROGTIN 169
      ::::::::::: :| :: ::| | :| | :| | ::
Db 112 GNGYISRSEMLEIYQAI-----YKAVSYWKMPEDESTPEKRTDKIFRQMDINNDKLS 165
      ::::::::::: :| :: ::| | :| | :| | ::

QY 170 LSEF-----QHVISRSPDFASSF 187
      ||| ::| | |||
Db 166 LEEFIKGAKSDEPSIVRLLOCDPSSASQF 193

```

RESULT 15
US-09-048-889-1

; Sequence 1, Application US/09048889
; Patent No. 6117989

GENERAL INFORMATION:

APPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer L.

APPLICANT: Corley, Nell C.
APPLICANT: Guegler, Karl J.

APPLICANT: Lal, Preeti

```

; APPLICANT: Patterson, Chandra
; TITLE OF INVENTION: HUMAN CALCIUM-BINDING PROTEINS
; NUMBER OF CLAIMS: 1

```

```

; NUMBER OF SEQUENCES: 1.
; CORRESPONDENCE ADDRESS:

```

ADDRESSEE: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Drive
CITY: Palo Alto

STATE: CA
COUNTRY: USA
STD: 04204

```

;      ZIP:  94304
;      COMPUTER READABLE FORM:
;      VEDTIV:  FIRST

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MEDIUM TYPE: Diskette

COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: Pro4Sec for Win

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; SOFTWARE: FASTSEQ FOR WINDOWS Version 2.0
;
; CURRENT APPLICATION DATA:
;
; APPLICATION NUMBER: ITS/00/000 000

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APPLICATION NUMBER: US/09/048,883
FILING DATE: Herewith
CLASSIFICATION:

```

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:

```

ATTORNEY/AGENT INFORMATION.

```

; AIRCRAFT/AGENT INFORMATION:
; NAME: Cerrone, Michael C
; REGISTRATION NUMBER: 20 1

```

REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0493 US
TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166

TELEFAX: 030-843-4166
TELEX:
INFORMATION FOR SEO ID NO. 1

```

; INFORMATION FOR SEQ ID NO:
;
; SEQUENCE CHARACTERISTICS:
;
; LENGTH: 186 aa (10,345

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LENGTH: 196 amino acids
TYPE: amino acid
STRANDNESS: single

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; SIKANDEDNESS: single
; TOPOLOGY: linear
.. IMMEDIATE SOURCE.

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IMMEDIATE SOURCE:
LIBRARY: COLNNOT09
CONE: 1946517

CLONE: 1840517
US-09-048-889-1

Query Match	14.8%;	Score 133.5;	DB 3;	Length 196;
Best Local Similarity	20.6%;	Pred. NO. 2.5e-06;		
Matches 39;	Conservative 48;	Mismatches 69;	Indels 33;	Gaps 6;

QY 5 GSRLSKELLAEYQD-----TFLTKQELLAAHRRFCCELLPOEQRVVSSLRAQVPEEQITLS 60
||| | : | : : : ||
DB 2 GSRTSHAAVIPDGSIRRETGFSQASLRLHRR-----BALDRNKKGYLSRMDLQ 53

```

01 LPELKANPFERICRVSTSTPAKDSLSFEDFLDLSTVF-----SDATPDIKS----- 108
      : | | | | | : | | : | : | : | | | |
54 IGAIAVNPGLGDRIIESFFPG-GSQRVDFPGFVRVLAHRRVEDEDETETQDPKKPELNSR 112
Db

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Search completed: January 17, 2003, 12:52:39
Job time : 16 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 17, 2003, 12:51:00 ; Search time 11 Seconds
(without alignments)
345.163 Million cell updates/sec

Title: US-09-878-454A-2X

Perfect score: 904
Sequence: 1 MGSGSRLSKELLA EYQDLT.....EFQHVISRSPDFASSFKIVL 191

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 120991 seqs, 19878514 residues

Total number of hits satisfying chosen parameters: 120991

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published_Applications_AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
- 10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
- 12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
- 13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
- 14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	904	100.0	191	US-09-878-454A-2	Sequence 2, Appli
2	892	98.7	191	US-10-109-885-2	Sequence 2, Appli
3	336	37.2	187	US-09-802-116-2	Sequence 2, Appli
4	171.5	19.0	170	US-10-109-885-3	Sequence 3, Appli
5	161.5	17.9	195	US-09-999-602-3	Sequence 3, Appli
6	157.5	17.4	195	US-09-999-602-4	Sequence 4, Appli
7	134	14.8	214	US-09-999-602-1	Sequence 1, Appli
8	126	13.9	220	US-09-350-874-26	Sequence 26, Appli
9	121	13.4	220	US-09-350-874-24	Sequence 24, Appli
10	121	13.4	252	US-09-350-874-20	Sequence 20, Appli
11	121	13.4	270	US-09-350-874-14	Sequence 14, Appli
12	118	13.1	270	US-09-350-874-18	Sequence 18, Appli
13	116	12.8	216	US-09-350-874-6	Sequence 6, Appli
14	116	12.8	225	US-09-350-874-30	Sequence 30, Appli
15	116	12.8	227	US-09-350-874-8	Sequence 8, Appli
16	116	12.8	227	US-09-350-874-10	Sequence 10, Appli
17	116	12.8	245	US-09-350-874-4	Sequence 4, Appli
18	116	12.8	252	US-09-350-874-22	Sequence 22, Appli
19	116	12.8	252	US-09-350-874-28	Sequence 28, Appli

20	116	12.8	252	10	US-09-350-874-42	Sequence 42, Appli
21	116	12.8	257	10	US-09-350-874-16	Sequence 16, Appli
22	115	12.7	216	9	US-09-965-528-15	Sequence 15, Appli
23	115	12.7	216	10	US-09-350-874-2	Sequence 2, Appli
24	107	11.8	229	10	US-09-350-874-70	Sequence 70, Appli
25	107	11.8	233	10	US-09-350-874-49	Sequence 49, Appli
26	107	11.8	250	10	US-09-350-874-72	Sequence 72, Appli
27	104.5	11.6	142	10	US-09-910-071-4	Sequence 4, Appli
28	104.5	11.6	172	12	US-10-109-885-4	Sequence 4, Appli
29	103	11.4	642	9	US-09-554-000-2	Sequence 2, Appli
30	103	11.4	642	9	US-09-554-000-6	Sequence 6, Appli
31	103	11.4	652	9	US-09-554-000-4	Sequence 4, Appli
32	103	11.4	656	9	US-09-554-000-8	Sequence 8, Appli
33	97.5	10.8	159	10	US-09-910-071-5	Sequence 5, Appli
34	96.5	10.7	1210	9	US-10-025-380-692	Sequence 692, Appli
35	96.5	10.7	1210	10	US-09-922-217-692	Sequence 692, Appli
36	96.5	10.7	1210	10	US-09-833-263-692	Sequence 692, Appli
37	96.5	10.7	1548	9	US-10-025-380-1095	Sequence 1095, Appli
38	96.5	10.7	1548	10	US-09-922-217-1095	Sequence 1095, Appli
39	96	10.6	256	10	US-09-350-874-32	Sequence 32, Appli
40	94.5	10.5	201	10	US-09-925-297-714	Sequence 714, Appli
41	92	10.2	256	10	US-09-350-874-36	Sequence 36, Appli
42	91.5	10.1	139	10	US-09-864-761-34808	Sequence 34808, Appli
43	91.5	10.1	1184	10	US-09-815-242-5229	Sequence 5229, Appli
44	91.5	10.1	1188	10	US-09-815-242-12125	Sequence 12125, Appli
45	91	10.1	330	9	US-09-870-759-82	Sequence 82, Appli

ALIGNMENTS

RESULT 1
US-09-878-454A-2
Sequence 2, Application US/09878454A
Patent No. US20020064828A1
GENERAL INFORMATION:
APPLICANT: Montelro, et al.
TITLE OF INVENTION: Method of Controlling the Binding of Calmyrin to Presentin1
FILE REFERENCE: 4115-161
CURRENT APPLICATION NUMBER: US/09/878,454A
PRIOR FILING DATE: 2001-06-11
PRIOR APPLICATION NUMBER: 60/210,939
PRIOR FILING DATE: 2000-06-11
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
LENGTH: 191
TYPE: PRT
ORGANISM: Homo sapiens
US-09-878-454A-2

Query Match 100.0%; Score 904; DB 10; Length 191;
Best Local Similarity 93.2%; Pred. No. 2.9e-78;
Matches 178; Conservative 13; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGSGSRLSKELLA EYQDLTFLTRQELLAHRRFCCLLPQEQRTVESSLRAQVPEQILS 60
Db 1 MGSGSRLSKELLA EYQDLTFLTRQELLAHRRFCCLLPQEQRTVESSLRAQVPEQILS 60
QY 61 LPELKANPEKERICRVFSTSPAKDSLSFEDFLDLVSFSDTATPDIKSHYAFRIPIXXXX 120
Db 61 LPELKANPEKERICRVFSTSPAKDSLSFEDFLDLVSFSDTATPDIKSHYAFRIPIDDDD 120
QY 121 XXXXXXXXSRVNLCTGEGEDTRLSASEMKOLIDNILESDIDRDGTINLSEFQHVISR 180
Db 121 GTLNREDLSRLVNLCTGEGEDTRLSASEMKOLIDNILESDIDRDGTINLSEFQHVISR 180
QY 181 PDFASSFKIVL 191
Db 181 PDFASSFKIVL 191

RESULT 2

US-10-109-885-2
; Sequence 2, Application US/10109885
; Patent No. US20020119129A1
; GENERAL INFORMATION:
; APPLICANT: REVEL, Michel
; APPLICANT: CHEBATH, Judith
; APPLICANT: ABRAMOVITCH, Carolina
; TITLE OF INVENTION: NOVEL IFN RECEPTOR I BINDING PROTEIN, DNA ENCODING THEM, AND METH
; TITLE OF INVENTION: MODULATING CELLULAR RESPONSE TO INTERFERON
; FILE REFERENCE: REVEL-14A
; CURRENT APPLICATION NUMBER: US/10/109,885
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: US/09/341,640
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: PCT/US98/00671
; PRIOR FILING DATE: 1998-01-15
; PRIOR APPLICATION NUMBER: US 60/035,636
; PRIOR FILING DATE: 1997-01-15
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 191
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-109-885-2
Query Match 98.7%; Score 892; DB 12; Length 191;
Best Local Similarity 92.1%; Pred. No. 4e-77;
Matches 176; Conservative 14; Mismatches 1; Indels 0; Gaps 0;
QY 1 MGGSGRSLSKELLAAYQDLTFLTKQEIILAHRRFCELLPQEQRTVSSSLRAQVPEQILS 60
Db 1 MGGSGRSLSKELLAAYQDLTFLTKQEIILAHRRFCELLPQEQRSVSSSLRAQVPEQILS 60
QY 61 LPKLANPFEKRICRVFSTSPAKDSLSFEDFLDLSVFSDTATPDIKSHYAFRIEXXXXX 120
Db 61 LPKLANPFEKRICRVFSTSPAKDSLSFEDFLDLSVFSDTATPDIKSHYAFRIEDFDD 120
QY 121 XXXXXXXXSRSLVNLCTGEGEDTRLSASEMKQLIDNILEESDIDRDGTINLSEFQHV 180
Db 121 GTLNREDLSRLVNLCTGEGEDTRLSASEMKQLIDNILEESDIDRDGTINLSEFQHV 180
QY 181 PDFASSFKIVL 191
Db 181 PDFASSFKIVL 191
RESULT 3
US-09-802-116-2
; Sequence 2, Application US/09802116
; Patent No. US20020082406A1
; GENERAL INFORMATION:
; APPLICANT: Mathur, Brian
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. US20020082406A1el Human Kinase Interacting Protein and Polynu
; TITLE OF INVENTION: the Same
; FILE REFERENCE: LEX-0146-USA
; CURRENT APPLICATION NUMBER: US/09/802,116
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 60/187,719
; PRIOR FILING DATE: 2000-03-08
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 187
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-802-116-2
Query Match 37.2%; Score 336; DB 10; Length 187;
Best Local Similarity 37.8%; Pred. No. 3.1e-24;
Matches 73; Conservative 52; Mismatches 56; Indels 12; Gaps 5;

QY 1 MGGSGRSLSKELLAAYQDLTFLTKQEIILAHRRFCELLPQEQRTVSSSLRAQVPE 56
Db 1 MGNKQTVTFHEQLEAYQDCTFFTRKEIMRLEFVRYQDLAPQLVPLDYTTCPD--VKVPYE 57
QY 57 QILSLPELKANPFEKRICRVFSTSPAKDSLSFEDFLDLSVFSDTATPDIKSHYAFRIEX 116
Db 58 LIGSMPELKNDFRQRIAQVFS-EDGDGHTLDFNDFMSVMSEMAPRDLKAYAFKIYD 116
QY 117 XXXXXXXXSRSLVNLCTGEGEDTRLSASEMKQLIDNILEESDIDRDGTINLSEFQHV 176
Db 117 FNNDDYICAWDLEQTVTKLT-RGE---LSAEESVLCVKVLEADGDHGDHGRSLSEDFQNM 172
QY 177 ISRSPDFASSEFKI 189
Db 173 ILRAPDFELSTPHI 185
RESULT 4
US-10-109-885-3
; Sequence 3, Application US/10109885
; Patent No. US20020119129A1
; GENERAL INFORMATION:
; APPLICANT: REVEL, Michel
; APPLICANT: CHEBATH, Judith
; APPLICANT: ABRAMOVITCH, Carolina
; TITLE OF INVENTION: NOVEL IFN RECEPTOR I BINDING PROTEIN, DNA ENCODING THEM, AND
; TITLE OF INVENTION: MODULATING CELLULAR RESPONSE TO INTERFERON
; FILE REFERENCE: REVEL-14A
; CURRENT APPLICATION NUMBER: US/10/109,885
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: US/09/341,640
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: PCT/US98/00671
; PRIOR FILING DATE: 1998-01-15
; PRIOR APPLICATION NUMBER: US 60/035,636
; PRIOR FILING DATE: 1997-01-15
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-10-109-885-3
Query Match 19.0%; Score 171.5; DB 12; Length 170;
Best Local Similarity 27.0%; Pred. No. 1.1e-08;
Matches 33; Conservative 42; Mismatches 42; Indels 5; Gaps 2;
QY 56 EQILSLPELKANPFEKRICRVFSTSPAKDSLSFEDFLDLSVFSDTATPDIKSHYAFRI 115
Db 41 EEFMSLPELQQNPLVQRVIDFDTD-GNGEVDFKEFIEGVSVKGDKEQKLRFARIY 99
QY 116 XXXXXXXXSRSLVNLCTGEGEDTRLSASEMKQLIDNILEESDIDRDGTINLSEFQHV 175
Db 100 DMDKDGYSINGELFQVLKMMVG-----NNLKDQLQQLQIVDKTIINADKDGGRISFEFCA 155
QY 176 VI 177
Db 156 VW 157
RESULT 5
US-09-999-602-3
; Sequence 3, Application US/09999602
; Patent No. US20020091084A1
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti G.
; APPLICANT: Corley, Neil C.
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: HUMAN CALCIUM BINDING PROTEIN
; FILE REFERENCE: PF-0468-2 CON

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: CURRENT APPLICATION NUMBER: US/09/999,602
: CURRENT FILING DATE: 2001-10-25
: PRIOR APPLICATION NUMBER: 09/010,378
: PRIOR FILING DATE: 1998-01-21
: NUMBER OF SEQ ID NOS: 4
: SOFTWARE: PERL Program
: SEQ ID NO 3
: LENGTH: 195
: TYPE: PRT
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: OTHER INFORMATION: Incyte ID No. US20020091084A1 g1226242
US-09-999-602-3

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Query Match          17.98% Score 161.5; DB 10; Length 195;
Best Local Similarity 24.1%; Pred. No. 1.3e-07;
Matches 47; Conservative 45; Mismatches 74; Indels 29; Gaps 6;

QY      1 MGGSGSRLSK-ELLAEXODITFLTKQEILLAHRRFCCELLPQEQRTVESSLRAQVPFEQIL 59
      11  | | : | | | : | : | : | | | | : |
Db      1 MGSRASTLLRDELELEIKKEGTGFSSHQITRLYSRFTSLDKGENGTLNR-----EDFQ 52
QY      60 SLPELKANPFKERICRVESTSPAKDSLSFEDFLDLLSVF-----SDTATPD----- 105
      : | | | | : | | | | : | : | | : | : | | : |
Db      53 RIPELAINPLGDRILINAF-FSEGEDQVNFGRGFMRTLAHFRPIEDNEKSKDVNGPEPLNSR 111
QY      106 -IKSHYAFRIEXXXXXXXXXXXXXSRVLVNCLTGEGEDTRLASSEMKQOLIDNILEESDIDR 164
      | | : | | | : : : : : : : : : : : : : : : |
Db      112 SNKLFHAFRLYDLDKRDCKISRDELLQVLRMMVG-----VNISDEQLGSIADRTIQEADQDG 167
QY      165 DGTINLSEFQHVIVSR 179
      | | : | | | : : :
Db      168 DSAISFTFEFVKVLEK 182

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RESULT 6
US-09-999-602-4
; Sequence 4, Application US/099999602
; Patent No. US20020091084A1
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti G.
; APPLICANT: Corley, Neil C.
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: HUMAN CALCIUM BINDING PROTEIN
; FILE REFERENCE: PF-0468-2 CON
; CURRENT APPLICATION NUMBER: US/09/999,602
; CURRENT FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: 09/010,378
; PRIOR FILING DATE: 1998-01-21
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PERL Program
; SEQ ID NO 4
; LENGTH: 195
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20020091084A1 g1706967
US-09-999-602-4

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Query Match          17.48;  Score 157.5;  DB 10;  Length 195;
Best Local Similarity 23.68;  Pred. No. 3.2e-07;
Matches 46;  Conservative 45;  Mismatches 75;  Indels 29;  Gaps 6;

QY      1  MGGSGSRLSK-ELLAEXODLTFLLTKOEILLAHRRFCCELLPQEQRTVESSLRAQVPFEQIL 59
      ||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db      1  MGSRASTLLRDELEETIKETGFSHSQITRLYSRFTSLDKGNGTLSR-----EDFQ 52

QY      60  SLPELKANPFKERICRYVESTSPAKDSLSEFEDLDLSVF-----SDTATPD----- 105
      :|||  ||  :|||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db      53  RIPELAINPLGDRINAAFPPE-GEDQVNFRCGFMRITLAHFRPIEDNEKSKDVNGPEPLNSR 111

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QY 106 -IKSHYAFRIEXXXXXXXXXXXXXSRLVNCLTGEGEDTRLASASEMKOLIDNILEESDIDR 164
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Db 112 SNKLHFAFRLYDLDKDEKISRDELLQVLRMMVG---VNISDEQLGSIADRTIQEADQDG 167
    | | : | | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : |
QY 165 DGTINLSEFQHVISR 179
    | | : : | | : : :
Db 168 DSAISFTTEFVKYLEK 182
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RESULT 7
US-09-999-602-1
; Sequence 1, Application US/09999602
; Patent No. US20020091084A1
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti G.
; APPLICANT: Corley, Neil C.
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: HUMAN CALCIUM BINDING PROTEIN
; FILE REFERENCE: PF-0468-2 CON
; CURRENT APPLICATION NUMBER: US/09/999,602
; CURRENT FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: 09/010,378
; PRIOR FILING DATE: 1998-01-21
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PERL Program
; SEQ ID NO 1
; LENGTH: 214
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20020091084A1 134682
US-09-999-602-1

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	Query Match	14.88;	Score 134;	DB 10;	length 214;	
	Best Local Similarity	22.7%;	Pred. No.	6.5e-05;		
	Matches 42;	Conservative 39;	Mismatches 50;	Indels 54;	Gaps 6;	
OY	1 MGGSGSRLSKELLAEYO D LFTLTQKEILLAHRRFCCELLPOEORTVESSLRAQVPFEQLS	60				
Dd	1 MGAHS--ASEEVRELKGTGTFSSDQIEOLHRRF-KQLSDGPPIRK-----ENFNN	49				
OY	61 LPELKANPFKERICRVF-----STSPAKDSLSEDFDLDSVSDTATPDIKSHYA	F 112				
Dd	50 VPDLELPNIRSKIYRAFEDNRNLKRGPSGLADEINFEDFLIMSYR-----	96				
OY	113 RIFXXXXXXXXXXXXXSVNCLTGEGEDTRLASASEMKQLIDNILLESDIDRDGTINLS	E 172				
Dd	97 ---PIDTMDEEQVELSR-----KENLRFLFMHYDDSDSDGRITLEE	I 134				
OY	173 FQHVI	177				
Dd	135 YRNIV	139				

RESULT 8
US-09-350-874-26
: Sequence 26, Application US/09350874
: Patent No. US20020019020A1
: GENERAL INFORMATION:
: APPLICANT: Rhodes, Kenneth
: APPLICANT: An, Wenqian
: TITLE OF INVENTION: METHODS FOR TREATING CARDIOVASCULAR DISORDERS
: FILE REFERENCE: MNI-069
: CURRENT APPLICATION NUMBER: US/09/350, 874
: CURRENT FILING DATE: 1999-07-09
: EARLIER APPLICATION NUMBER: USSN 60/110,277
: EARLIER FILING DATE: 1998-11-30
: EARLIER APPLICATION NUMBER: USSN 60/110,033
: EARLIER FILING DATE: 1998-11-25
: EARLIER APPLICATION NUMBER: USSN 60/109,333
: EARLIER FILING DATE: 1998-11-20
: EARLIER APPLICATION NUMBER: USSN 09/298,731

SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 14
 LENGTH: 270
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-350-874-14

Query Match 13.4%; Score 121; DB 10; Length 270;
 Best Local Similarity 20.7%; Pred. No. 0.0017;
 Matches 38; Conservative 55; Mismatches 77; Indels 14; Gaps 5;

QY 11 ELLAEYQDLTFLTKQEILLAHRRFCCELLPQEQRTVESSLRAQVPEQILS--LPCLKANP 68
 DB 91 EGLEQLQEQTKFTRKELQVLYRGFKNECP-----SGIVNEENFKQIYSQFFPQGDSSST 143
 QY 69 EKERICRVSTSPAKDSLSEFDLIDLVSFSDTATPDIKSHYAFRIEXXXXXXXX 128
 DB 144 YATFLFNADTN-HDGSVSFEDFVAGLSVIL-RGTVDRLNMAFNLYDLNKDGCITKEEM 201
 QY 129 SRLVNC--LTGEGEDTRLASASEMKOLIDNILESDIDRDGTINLSEFQHVISRSPDFAS 185
 DB 202 LDIMKSIYDMGKYTPALREAPREHVESFQKMDRNKDGVTIEEFIESQKDENIMR 261
 QY 186 SFKI 189
 DB 262 SMQL 265

RESULT 12
 US-09-350-874-18
 Sequence 18, Application US/09350874
 Patent No. US20020019020A1
 GENERAL INFORMATION:
 APPLICANT: Rhodes, Kenneth
 TITLE OF INVENTION: METHODS FOR TREATING CARDIOVASCULAR DISORDERS
 FILE REFERENCE: MNI-069
 CURRENT APPLICATION NUMBER: US/09/350,874
 EARLIER FILING DATE: 1999-07-09
 EARLIER APPLICATION NUMBER: USSN 60/110,277
 EARLIER FILING DATE: 1998-11-30
 EARLIER APPLICATION NUMBER: USSN 60/110,033
 EARLIER FILING DATE: 1998-11-25
 EARLIER APPLICATION NUMBER: USSN 60/109,333
 EARLIER FILING DATE: 1998-11-20
 EARLIER APPLICATION NUMBER: USSN 09/298,731
 EARLIER FILING DATE: 1999-04-23
 NUMBER OF SEQ ID NOS: 72
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 18
 LENGTH: 270
 TYPE: PRT
 ORGANISM: Mus musculus
 US-09-350-874-18

Query Match 13.1%; Score 118; DB 10; Length 270;
 Best Local Similarity 22.0%; Pred. No. 0.0033;
 Matches 37; Conservative 51; Mismatches 66; Indels 14; Gaps 5;

QY 11 ELLAEYQDLTFLTKQEILLAHRRFCCELLPQEQRTVESSLRAQVPEQILS--LPCLKANP 68
 DB 91 EGLEQLQEQTKFTRKELQVLYRGFKNECP-----SGIVNEENFKQIYSQFFPQGDSSN 143
 QY 69 EKERICRVSTSPAKDSLSEFDLIDLVSFSDTATPDIKSHYAFRIEXXXXXXXX 128
 DB 144 YATFLFNADTN-HDGSVSFEDFVAGLSVIL-RGTIDRLNMAFNLYDLNKDGCITKEEM 201
 QY 129 SRLVNC--LTGEGEDTRLASASEMKOLIDNILESDIDRDGTINLSEF 173
 DB 202 LDIMKSIYDMGKYTPALREAPREHVESFQKMDRNKDGVTIEEF 249
 RESULT 13

US-09-350-874-6
 Sequence 6, Application US/09350874
 Patent No. US20020019020A1
 GENERAL INFORMATION:
 APPLICANT: Rhodes, Kenneth
 TITLE OF INVENTION: METHODS FOR TREATING CARDIOVASCULAR DISORDERS
 FILE REFERENCE: MNI-069
 CURRENT APPLICATION NUMBER: US/09/350,874
 CURRENT FILING DATE: 1999-07-09
 EARLIER APPLICATION NUMBER: USSN 60/110,277
 EARLIER FILING DATE: 1998-11-30
 EARLIER APPLICATION NUMBER: USSN 60/110,033
 EARLIER FILING DATE: 1998-11-25
 EARLIER APPLICATION NUMBER: USSN 60/109,333
 EARLIER FILING DATE: 1998-11-20
 EARLIER APPLICATION NUMBER: USSN 09/298,731
 EARLIER FILING DATE: 1999-04-23
 NUMBER OF SEQ ID NOS: 72
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 6
 LENGTH: 216
 TYPE: PRT
 ORGANISM: Mus musculus
 US-09-350-874-6

Query Match 12.8%; Score 116; DB 10; Length 216;
 Best Local Similarity 22.6%; Pred. No. 0.0034;
 Matches 38; Conservative 43; Mismatches 73; Indels 14; Gaps 5;

QY 11 ELLAEYQDLTFLTKQEILLAHRRFCCELLPQEQRTVESSLRAQVPEQILS--LPCLKANP 68
 DB 37 EGLEQLQEQTKFTRKELQVLYRGFKNECP-----SGIVNEENFKQIYAQFFPHGDAST 89
 QY 69 EKERICRVSTSPAKDSLSEFDLIDLVSFSDTATPDIKSHYAFRIEXXXXXXXX 128
 DB 90 YAHYLFNADTQF-GSVKFEDFVAPALISLL-RGTVHEKLRMTFNLYDINKDGYINKKEEM 147
 QY 129 SRLVNC--LTGEGEDTRLASASEMKOLIDNILESDIDRDGTINLSEF 173
 DB 148 MDIVKAIYDMGKYTPVLKEDTPRQHYDVFFQKMDKNKDGIVTLDEF 195

RESULT 14
 US-09-350-874-30
 Sequence 30, Application US/09350874
 Patent No. US20020019020A1
 GENERAL INFORMATION:
 APPLICANT: Rhodes, Kenneth
 TITLE OF INVENTION: METHODS FOR TREATING CARDIOVASCULAR DISORDERS
 FILE REFERENCE: MNI-069
 CURRENT APPLICATION NUMBER: US/09/350,874
 CURRENT FILING DATE: 1999-07-09
 EARLIER APPLICATION NUMBER: USSN 60/110,277
 EARLIER FILING DATE: 1998-11-30
 EARLIER APPLICATION NUMBER: USSN 60/110,033
 EARLIER FILING DATE: 1998-11-25
 EARLIER APPLICATION NUMBER: USSN 60/109,333
 EARLIER FILING DATE: 1998-11-20
 EARLIER APPLICATION NUMBER: USSN 09/298,731
 EARLIER FILING DATE: 1999-04-23
 NUMBER OF SEQ ID NOS: 72
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 30
 LENGTH: 225
 TYPE: PRT
 ORGANISM: Rattus sp.
 US-09-350-874-30

Query Match 12.8%; Score 116; DB 10; Length 225;
 Best Local Similarity 22.0%; Pred. No. 0.0037;
 Matches 37; Conservative 50; Mismatches 67; Indels 14; Gaps 5;

RESULT 15

	Query Match	12.8%;	Score 116;	DB 10;	Length 227;
	Best Local Similarity	22.6%;	Pred. NO. 0.0037;		
	Matches 38;	Conservative 43;	Mismatches 73;	Indels 14;	Gaps 5;
QY	11	ELLA EYQDLTFLTKQEILLAHRRFCCELLPQEQRTVESSLRAQVPFEQILS--LPELKANP	68		
Db	48	EGLEQLEAQTNFKRELQVLYRGFKNECP-----SGVVNEETFKQIYAQFFPHGDAST	100		
QY	69	FKERICRVFSTSPAKDSLSFEDFLDLLSVFSDTATPDIKSHYAFRIFXXXXXXX	128		
Db	101	YAHYLFNAFDITQT-GSVKFEDFVTALSILL-RGTVHEKLRWTFNLYDINKDGYINKEEM	158		
QY	129	SRLVNC---LTGEGEDTRLASSEMKQLIDNILEESDIDRDGTINLSEF	173		
Db	159	MDIVKAIYDMGKYTYPVLKEDTPRQHVDFYFQKMDKNKDGIIVTLDEF	206		

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Job time : 12 secs

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OM protein - protein search, using sw model

Run on: January 17, 2003, 12:50:00 ; Search time 16 Seconds
(without alignments)
1147.605 Million cell updates/sec

Title: US-09-878-454A-2X
Perfect score: 904
Sequence: 1 MGSGSGRLSKELLAERYQDLT.....EFQHVISRSPDFASSFKIVL 191

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. NO. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	393	43.5	311	2	T21563	hypothetical prote
2	196.5	21.7	174	2	T41632	probable calcineur
3	189.5	21.0	175	2	JH0462	phosphoprotein pho
4	185.5	20.5	174	2	T47245	calcineurin regula
5	171.5	19.0	170	1	A33391	calcineurin regula
6	171.5	19.0	170	1	S34127	calcineurin regula
7	171.5	19.0	170	1	JC1220	calcineurin regula
8	171.5	19.0	216	1	S42716	calcineurin regula
9	169.5	18.8	369	2	T22708	hypothetical prote
10	165.5	18.3	195	2	T28047	hypothetical prote
11	164.5	18.2	213	2	T31775	hypothetical prote
12	161.5	17.9	170	2	JC5174	calcineurin regula
13	160.5	17.8	170	2	JC7242	calcineurin regula
14	157.5	17.4	170	2	A44307	calcineurin regula
15	156.5	17.3	226	2	T51357	calcineurin regula
16	155.5	17.2	179	2	JC1221	calcineurin regula
17	153.5	17.0	165	2	PS0261	calcineurin regula
18	153.5	17.0	176	2	J01232	calcineurin regula
19	148.5	16.4	190	2	T20725	calcineurin regula
20	146	16.2	192	2	T01375	hypothetical prote
21	144.5	16.0	226	2	T08923	calcineurin B-like
22	142	15.7	246	2	T05308	hypothetical prote
23	142	15.7	246	2	H85387	hypothetical prote
24	140.5	15.5	213	2	T51356	calcineurin B-like
25	138	15.3	193	2	T50676	gene Rem-1 protein
26	137	15.2	224	2	F96668	protein FIN19.5 [1
27	136	15.0	193	2	JH0816	neural vistin-lik
28	135	14.9	190	2	I51686	frequency - Africa
29	135	14.9	193	2	S47565	calcium-binding pr

30	128	14.2	190	2	A55666
31	125	13.8	191	2	JH0815
32	124	13.7	193	2	JH0616
33	122.5	13.6	155	2	S38877
34	122.5	13.6	172	2	S38531
35	121	13.4	190	2	S58303
36	121	13.4	190	2	S61168
37	121	13.4	172	2	JC7631
38	119.5	13.2	172	2	I38424
39	119	13.2	214	2	T08922
40	118.5	13.1	254	2	T29566
41	118	13.1	193	2	JC2186
42	117.5	13.0	158	2	A38397
43	117	12.9	151	2	A71409
44	116.5	12.9	155	2	S38878
45	116	12.8	791	2	A53691

neurocalcin - fru
neural vistin-lik
neurocalcin (clone
tropoin C isoform
caltractin - mouse
related to neuona
hypothetical prote
K+ channel-interac
centrin - human
hypothetical prote
hypothetical prote
hippocalcin - huma
tropoin C-1 - gila
calmodulin 8 [lmpo
tropoin C isoform
diacylglycerol kin

ALIGNMENTS

RESULT 1
T21563
hypothetical protein F30A10.1 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C/Accession: T21563
R:Barlow, K.
submitted to the EMBL Data Library, October 1996
A/Reference number: Z19442
A/Accession: T21563
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-311 <WT>
A/Cross-references: EMBL:Z81072; PIDN:CAB03019.1; GSPDB:GN00019; CESP:F30A10.1
A/Experimental source: clone F30A10
C/Genetics:
A/Gene: CESP:F30A10.1
A/Map position: 1
A/Introns: 106/2; 139/3; 190/3; 240/1

Query Match 43.5%; Score 393; DB 2; Length 311;
Best Local Similarity 39.6%; Pred. No. 3.8e-21;
Matches 82; Conservative 52; Mismatches 47; Indels 26; Gaps 5;

QY 1 MGSGSGRLS-----KELLAERYQDLTFLTKQELLAHRCCELLPQORTVESS 48
DB 111 MGNMSSLSSENLFSKGVFTREQDDEYQDCTFTTRKDITRLRYKRYALNPHK--VPTN 167
QY 49 LRAQVP-----FEQILSLPELKANPFKERICRVFSTSPAKSLSFEDFLDLVSFSDTA 102
DB 168 MGNRPATITTLTFEEVEKMPELKENPFKRRICEVFS-EDGRNLSFDDELDFMFSVFSMA 226
QY 103 TPDIKSHYAFRIFFXXXXXXXSRVNLCTGEGEDTRLSASEMKOLIDNILESDI 162
DB 227 PLQLKRYAFRIYDYDDELGHDDLSKMIRSLTRD---ELSDVEVEFIERIEEADL 282
QY 163 DRDGTINLSEFQHVISRSPDFASSFKI 189
DB 283 DGDSSINFAEFHVSRSRSPDFIRTFHI 309

RESULT 2
T41632
probable calcineurin b subunit - fission yeast (Schizosaccharomyces pombe)
C/Species: Schizosaccharomyces pombe
C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 04-Feb-2000
C/Accession: T41632
R/McDougall, R.M.; Rajandream, M.A.; Barrell, B.G.; Ramsperger, U.; Pohl, T.
submitted to the EMBL Data Library, August 1999
A/Reference number: Z22005
A/Accession: T41632
A/Status: preliminary; translated from GB/EMBL/DBJ


```

Db      1  MGNSSSLMRDEIEIEIMSETEFNRNQIVRLYSRFLSLDKKGQGFLSR-----DDFL 52
QY      60  SLPELKANPEFKERICRVFSTSPA-----KDSLSEFEDFLDLVSFSDTATPDIKSH---- 109
      :||| | : || | | : : || | | : || : || :
Db      53  NYPELAVNPLGDRIVDAFFTLASSNGDNEEQQLNRFQVARIHAHQPISR--VKKNALNS 110
QY      110 -----YAFRIFXXXXXXXXXXXXXSRVLVNCLTGEGEDPTRISASEMKQOLIDNILEESDID 163
      :||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      111  RKDKLLFAFKMYIDLKNDYITTREEFKVILNSMWG---ANITSQDLKIADRTIEEADAD 166
QY      164  RDGTINLSEFQHVISR 180
      ||| | : || : : :
Db      167  RDGKISFDEFCEFRAMEKT 183

```

```

RESULT 11
T31775
hypothetical protein F59D6.7 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C:Accession: T31775
R:Bradshaw, H.; Graves, T.
submitted to the EMBL Data Library, July 1997
A:Description: The sequence of C. elegans cosmid F59D6.
A:Reference number: 221083
A:Accession: T31775
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-213 <BRA>
A:Cross-references: EMBL:AF016435; PIDN:AAB65882.1; GSPDB:GN00023; CESP:F59D6.7
A:Experimental source: strain Bristol N2; clone F59D6
C:Genetics:
A:Gene: CESP:F59D6.7
A:Map position: 5
A:Introns: 24/2; 60/1; 135/1

```

```
Query Match              18.2%; Score 164.5; DB 2; Length 213;  
Best Local Similarity   22.1%; Pred. No. 0.00013;  
Matches    47; Conservative    53; Mismatches    68; Indels    45; Gaps      7;
```

```
QY     1 MGSGSRL-----SKELLAEQ-----DLTFLTKQEILLAHRCCELLPQE 41  
       || | :          :||| | |           : |:|| . : || |  
Db     1 MGNSSNLSLDAEMREIMDETQQKVCVLIAKQTTPKNITSVNKHQILRLYTRFASL---- 56  
  
QY     42 QRTVESSLRAQVPFEQIILSLPELKANPFKERICRVESTSPAKD-----SLSFEDFDLL 95  
       : : : : : : :||::||| || :|| | | | |         :|| | :|| |  
Db     57 ----DKNGGGYLSRDDFLNPVELAVNPPLGDRITIIDAFFILIIGDSGDGSDSKSGQLTFROFVRIL 112  
  
QY     96 SVF-----SDTATPDIKS--HYAFRIFXXXXXXXXXXXXXXSRVLVNCLTGEGEDTRLAS 147  
       : |          | | | | | | | | | | | | | | | | | :|| :|| :|| :||  
Db     113 AHFOPISTKVKDNALNSRKDKLRPAFKMYIDLNNNYITREEFKVILNSMWG---ANTISD 168  
  
QY     148 EMKOLIDNILEESDIDRDGTINLSEFOHVISRS 180  
       :: : : | ||| :||| || : : : :  
Db     169 OLDKIADKTLEEAQQDRDGKISFEDEFCRAMEKT 201
```

RESULT 12
JC5174
calcineurin regulatory chain 2 - fruit fly (*Drosophila melanogaster*)
N:Alternate names: calcineurin beta subunit; calcineurin chain B-2; phosphoprotein phosph
C:Species: *Drosophila melanogaster*
C:Date: 16-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 13-Aug-1999
C:Accession: JC5174
R:Warren, W.D.; Phillips, A.M.; Howells, A.J.
Gene 177, 149-153, 1996
A:Title: *Drosophila melanogaster* contains both X-linked and autosomal homologues of the
A:Reference number: JC5174; MUID:97080515; PMID:8921860
A:Accession: JC5174
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-170 <WAR>
A:Cross-references: GB:U56245; NID:g1336009; PIDN:AAC47350.1; PID:g1336010

C;Comment: This protein is the calcium binding chain of calcineurin, involved in c
C;Genetics:
A;Gene: dCnB2
C;Complex: heterodimer with calcineurin catalytic chain
C;Superfamily: calmodulin; calmodulin repeat homology
C;Keywords: blocked amino end; calcium binding; duplication; EF hand; heterodimer;
F;2-170/Product: calcineurin regulatory chain #status predicted <MAT>
F;18-49/Domain: calmodulin repeat homology <EF1>
F;50-82/Domain: calmodulin repeat homology <EF2>
F;87-119/Domain: calmodulin repeat homology <EF3>
F;128-160/Domain: calmodulin repeat homology <EF4>
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;3/Modified site: aspartic acid (Asn) #status predicted

[illegible]

RESULT 13
JC7242
calciineurin regulatory subunit, calciineurin B - scallop (Patinopecten yessoensis)
N:Alternate names: Ca2+/calmodulin-dependent phosphoprotein phosphatase regulatory
C:Species: Patinopecten yessoensis (Yesso scallop)
C:Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 21-Jul-2000
C:Accession: JC7242; PC7070
R:Uryu, M.; Nakatomi, A.; Watanabe, M.; Hatsuse, R.; Yazawa, M.
J.Biochem. 127, 739-746, 2000
A:Title: Molecular cloning of cDNA encoding two subunits of calciineurin from scallop
A:Reference number: JC7241
A:Accession: JC7242
A:Molecule type: mRNA
A:Residues: 1-170 <URX>
A:Cross-references: DDBJ:AB041524
A:Experimental source: testis
A:Accession: PC7070
A:Molecule type: protein
A:Residues: 12-68;73-85;92-170 <UR2>
C:Comment: This protein, one of Ca2+/calmodulin-dependent enzyme, is a testis-spec.
to the regulation of flagellar motility.

C;Superfamily: calmodulin; calmodulin repeat homology
C;Keywords: calcium binding; EF hand; flagellar rotation; myristylation; phosphoprote

```
Query Match          17.8%; Score 160.5; DB 2; Length 170;  
Best Local Similarity 22.3%; Pred. No. 0.00019;  
Matches    39; Conservative   51; Mismatches   66; Indels   19; Gaps    4;
```

QY 3 GSGSRSLKELLAEYQDLFLTRQEILLAHRRFCCELLPQEQRTVESSLRAQVPEQILSLP 62
 11::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |
Db 2 GNENSLPMELCSNFD-----PDEIKRLGKR-----KKLDLNGSGLSVDEFMTLP 47

QY 63 ELKANPFKERICRVFSTSPAKDSLSEDFDLDSVFSDTATPDIKSHYAFTIRXXXXXXX 122
 11::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |
Db 48 ELCQNPLVQRVIDIFDITD-NGGEVDVFKEFTIEGVQSFSVKDKLSKLRFARFIYDMKDGY 106

QY 123 KXXXXXSRVLNCLTGEGETRRLSASEMKOLIDNILEESDIDRDGTINLSEFOHVI 177
 :::::::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |
Db 107 ISNGELFOVLKMNVG---NNLKDTQLQQIVDKTIHADADGDGKISFEECNAVY 157

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 17, 2003, 12:49:14 ; Search time 13 Seconds

(without alignments)
609.383 Million cell updates/sec

Title: US-09-878-454A-2X

Perfect score: 904
Sequence: 1 MCGSGSRLSKELLAEXQDLT.....EFQHVISRSPDFASSFKIVL 191

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	904	100.0	191	1 KIP1_HUMAN	Q99828 homo sapien
2	856	94.7	191	1 KIP1_MOUSE	Q920f4 mus musculu
3	855	94.6	191	1 KIP1_RAT	Q9r010 rattus norv
4	326	36.1	187	1 KIP2_MOUSE	Q92309 mus musculu
5	324	35.8	187	1 KIP2_HUMAN	O75838 homo sapien
6	201.5	22.3	177	1 CALB_NAEGR	P42322 naegleria g
7	196.5	21.7	174	1 CALB_SCHPO	Q9uu93 schizosacch
8	185.5	20.5	174	1 CALB_NEUCR	P87072 neurospora
9	184.5	20.4	174	1 CALB_YEAST	P25296 saccharomyc
10	171.5	19.0	169	1 CALB_HUMAN	P06705 homo sapien
11	171.5	19.0	169	1 CALB_MOUSE	Q63810 mus musculu
12	161.5	17.9	170	1 CALC_MOUSE	Q24214 drosophila
13	160	17.7	194	1 CA22_MOUSE	Q62877 mus musculu
14	157.5	17.4	170	1 CALB_DROME	P48451 drosophila
15	156	17.3	194	1 CA22_HUMAN	Q99653 homo sapien
16	155.5	17.2	178	1 CALC_MOUSE	Q63811 mus musculu
17	153.5	17.0	175	1 CALC_RAT	P28470 rattus norv
18	148.5	16.4	189	1 NCS2_CAEEL	P36609 caenorhabdi
19	146.5	16.2	186	1 FREQ_DROME	P37236 drosophila
20	134	14.8	214	1 TESC_HUMAN	Q96b62 homo sapien
21	133	14.7	190	1 APLC_APLCA	Q16981 aplysia cal
22	133	14.7	192	1 VIS3_CHICK	P42324 gallus gall
23	132.5	14.7	195	1 H520_HUMAN	O43745 homo sapien
24	131	14.5	192	1 VIS3_MOUSE	P35333 mus musculu
25	131	14.5	192	1 TESC_MOUSE	Q9jkl5 mus musculu
26	130	14.4	189	1 NCS1_HUMAN	P36610 homo sapien
27	130	14.4	189	1 NCS1_XENLA	Q91614 xenopus lae
28	130	14.4	192	1 VIS3_HUMAN	P37235 homo sapien
29	126	13.9	190	1 NCS1_CAEEL	P36608 caenorhabdi
30	125	13.8	192	1 NCAD_MOUSE	Q91x97 mus musculu
31	123	13.6	189	1 NCAD_DROME	P42325 drosophila
32	122.5	13.6	155	1 TPC2_DROME	P47948 drosophila
33	122.5	13.6	172	1 CATR_MOUSE	P41209 mus musculu

34	120	13.3	190	1 VIS2_RAT	P35332 rattus norv
35	119.5	13.2	172	1 CAT2_HUMAN	Q12798 homo sapien
36	119	13.2	192	1 NCAD_CHICK	Q12953 gallus gall
37	119	13.2	192	1 NCAD_HUMAN	P29554 homo sapien
38	118.5	13.1	155	1 TPC3_DROME	P47949 drosophila
39	117.5	13.0	158	1 TPC1_BALNU	P21797 balanus nub
40	117	12.9	804	1 KDBG_HUMAN	Q9y6t7 homo sapien
41	116	12.8	189	1 NCS1_SCHPO	Q09711 schizosacch
42	116	12.8	189	1 NCS1_YEAST	Q06389 saccharomyc
43	116	12.8	791	1 KDGG_HUMAN	P49619 homo sapien
44	115	12.7	192	1 HIPB_HUMAN	P32076 homo sapien
45	113.5	12.6	801	1 KDBG_RAT	P49621 rattus norv

ALIGNMENTS

RESULT 1
KIP1_HUMAN
ID KIP1_HUMAN STANDARD; PRT; 191 AA.
AC Q99828; 000735; 000693; Q99971; Q96J54;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Calcium and integrin-binding protein 1 (Calmyrin) (DNA-PKcs
DE Interacting protein) (Kinase interacting protein) (KIP) (CIB) (SNK
DE Interacting protein 2-28) (SRP2-28).
GN CIB1 OR PRKDCIP OR KIP OR CIB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
RP Yuan O.;
RT "SNK, a Ser/Thr protein kinase, associated proteins.";
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
[2]
SEQUENCE FROM N.A.
RX MEDLINE=98040126; PubMed=9372844;
RA Wu X., Lieber M.R.;
RT "Interaction between DNA-dependent protein kinase and a novel protein,
RT KIP.";
RL Mutat. Res. 385:13-20(1997).
[3]
SEQUENCE FROM N.A.
RC TISSUE=Fetal liver;
RX MEDLINE=97184102; PubMed=9030514;
RA Naik U.P., Patel P.M., Parise L.V.;
RT "Identification of a novel calcium-binding protein that interacts
RT with the integrin alpha1b cytoplasmic domain.";
RL J. Biol. Chem. 272:4651-4654(1997).
[4]
SEQUENCE FROM N.A.
RP MEDLINE=20284952; PubMed=10826701;
RX Hattori A., Seki N., Hayashi A., Kozuma S., Saito T.;
RT "Genomic structure of mouse and human genes for DNA-PKcs interacting
RT protein (KIP).";
RL DNA Seq. 10:415-418(2000).
[5]
SEQUENCE FROM N.A.
RP TISSUE=Cervix;
RC Strausberg R.;
RX Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
[6]
STRUCTURE BY NMR OF 9-191.
RX MEDLINE=20283154; PubMed=10822252;
RA Hwang P.M., Vogel H.J.;
RT "Structures of the platelet calcium- and integrin-binding protein and
RT the alpha1b-integrin cytoplasmic domain suggest a mechanism for
RT calcium-regulated recognition; homology modelling and NMR studies.";
RL J. Mol. Recognit. 13:83-92(2000).
-1- FUNCTION: MAY CONVERT THE INACTIVE CONFORMATION OF INTEGRIN ALPHA-

```
CC IIB/BETA3 TO AN ACTIVE FORM THROUGH THE BINDING TO THE INTEGRIN
CC CYTOPLASMIC DOMAIN.
CC -!- SUBUNIT: INTERACTS WITH THE HETERODIMERIC INTEGRIN ALPHA-
CC IIB/BETA3. INTERACTS WITH THE PROTEIN KINASES SNK AND WITH THE
CC REGION IMMEDIATELY UPSTREAM OF THE KINASE DOMAIN OF DNA-PK.
CC -!- TISSUE SPECIFICITY: UBIQUITOUS.
CC -!- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U83236; AAB39758.1; -
CC EMBL; U85611; AAB53387.1; -
CC EMBL; U82226; AAC51106.1; -
CC EMBL; AB021866; BAA36281.1; -
CC EMBL; BC000846; AAH00846.1; -
CC PDB; 1DGV; 08-DEC-99.
CC Genew; HGNC:16920; CIB1.
CC MIM; 602293; -
CC InterPro; IPR002048; EF-hand.
CC Pfam; PF00036; efhand; 2.
CC ProDom; PD000012; EF-hand; 1.
CC SMART; SM00054; EFh; 2.
CC PROSITE; PS00018; EF_HAND; 2.
CC Calcium-binding; Repeat; 3D-structure.
CC CA_BIND 116 127 EF-HAND 1 (POTENTIAL).
CC CA_BIND 161 172 EF-HAND 2 (POTENTIAL).
CC CA_BIND 44 44 T -> S (IN REF. 3 AND 5).
CC CONFLICT 44 44
CC SEQUENCE 191 AA; 21717 MW; 9AA6EA7897881E55 CRC64;
CC -----
CC Query Match 100.0%; Score 904; DB 1; Length 191;
CC Best Local Similarity 93.2%; Pred. No. 1.8e-61;
CC Matches 178; Conservative 13; Mismatches 0; Indels 0; Gaps 0;
CC -----
QY 1 MGGSGSRLSKELLAQYQDLTFLTKQEILLAHRRFCCLLPQEQRTVSSLRAQVPFEQILS 60
Db 1 MGGSGSRLSKELLAQYQDLTFLTKQEILLAHRRFCCLLPQEQRTVSSLRAQVPFEQILS 60
QY 61 LPULKANPFKERICRVFSTSPAKDSLSFEDFLDLSVFSDTATPDIKSHYAFRIFXXXXX 120
Db 61 LPULKANPFKERICRVFSTSPAKDSLSFEDFLDLSVFSDTATPDIKSHYAFRIFDXXX 120
QY 121 XXXXXXSRVNLCTGEGEDTRLSASEMKQLIDNILESDIDRDGTINLSEFQHVISR 180
Db 121 GTLNREDLSRVNCLTGEEDTRLSASEMKQLIDNILESDIDRDGTINLSEFQHVISR 180
QY 181 PDFASSFKIVL 191
Db 181 PDFASSFKIVL 191
RESULT 2
KIPL_MOUSE STANDARD; PRT; 191 AA.
AC Q920F4;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Calcium and integrin-binding protein 1 (Calmyrin) (DNA-PKcs
DE interacting protein) (Kinase interacting protein) (KIP) (CIB).
GN CIB1 OR PRKDCIP OR KIP OR CIB.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Kidney;
```

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RX MEDLINE=99069785; PubMed=9852683;
RA Seki N., Hayashi A., Abe M., Araki R., Fujimori A., Fukumura R.,
RA Hattori A., Kozuma S., Ohhira M., Hori T., Saito T.;
RT "Chromosomal assignment of the gene for human DNA-PKcs interacting
RT protein (KIP) on chromosome 15q25.3-q26.1 by somatic hybrid analysis
RT and fluorescence in situ hybridization.";
RL J. Hum. Genet. 43:275-277(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Fetal kidney;
RX MEDLINE=99160477; PubMed=10051332;
RA Saito T., Seki N., Hattori A., Hayashi A., Abe M., Araki R.,
RA Fujimori A., Fukumura R., Kozuma S., Matsuda Y.;
RT "Structure, expression profile, and chromosomal location of a mouse
RT gene homologous to human DNA-PKcs interacting protein (KIP) gene.";
RL Mamm. Genome 10:315-317(1999).
RN [3]
RP SEQUENCE FROM N.A.
RA Naik M.U., Naik U.P.;
RT "Cloning and tissue distribution of murine calcium and integrin
RT binding protein, CIB.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
CC -!- FUNCTION: MAY CONVERT THE INACTIVE CONFORMATION OF INTEGRIN ALPHA-
CC IIB/BETA3 TO AN ACTIVE FORM THROUGH THE BINDING TO THE INTEGRIN
CC CYTOPLASMIC DOMAIN (BY SIMILARITY).
CC -!- SUBUNIT: INTERACTS WITH THE HETERODIMERIC INTEGRIN ALPHA-
CC IIB/BETA3. INTERACTS WITH THE PROTEIN KINASES SNK AND WITH THE
CC REGION IMMEDIATELY UPSTREAM OF THE KINASE DOMAIN OF DNA-PK (BY
CC SIMILARITY).
CC -!- TISSUE SPECIFICITY: UBIQUITOUS.
CC -!- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AB006463; BAA74429.1; -
CC EMBL; AB017361; BAA36165.1; -
CC EMBL; AF173010; AAG38960.1; -
CC EMBL; AK010345; BAB26868.1; -
CC HSSP; Q99828; 1DGV.
CC MGD; MGI:1344418; C1b1.
CC InterPro; IPR002048; EF-hand.
CC Pfam; PF00036; efhand; 2.
CC ProDom; PD000012; EF-hand; 1.
```

DR SMART; SM00054; EFh; 2.
 DR PROSITE; PS00018; EF_HAND; 2.
 KW Calcium-binding; Repeat.
 FT CA_BIND 116 127 EF-HAND 1 (POTENTIAL).
 FT CA_BIND 161 172 EF-HAND 2 (POTENTIAL).
 SO SEQUENCE 191 AA; 21763 MW; C85B603A19F9D9AC CRC64;

Query Match 94.7%; Score 856; DB 1; Length 191;
 Best Local Similarity 88.0%; Pred. NO. 7.7e-58;
 Matches 168; Conservative 16; Mismatches 7; Indels 0; Gaps 0;

QY 1 MGSGSRLSKELLAEXODLTLTKOEILAHRRFCCLLPQEQRTVESSLRAQVPEQILS 60
 DB 1 MGSGSRLSKELLAEXODLTLTKOEILAHRRFCCLLPQEQRTVESSLRAQVPEQILS 60
 QY 61 LPELKANPFEKRICRVSTSPAKDSLSFEDFLDLVSFSDTATPDIKSHYAFRIFFXXXXX 120
 DB 61 LPELKANPFEKRICRVSTSPAKDSLSFEDFLDLVSFSDTATPDIKSHYAFRIFFDDDD 120
 QY 121 XXXXXXXXSRVNCNLTGEGEDTRLASASEMKQIDNILEESDIDRDGTINLSEFQHVISRS 180
 DB 121 GTLDREDSLRLVNCNLTGEGEDTRLASASEMKQIDNILEESDIDRDGTINLSEFQHVISRS 180
 QY 181 PDFASSFKIVL 191
 DB 181 PDFASSFKIVL 191

RESULT 3

KIP1_RAT
 ID KIP1_RAT STANDARD; PRT; 191 AA.
 AC Q9R010;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Calcium and integrin-binding protein 1 (Calmyrin) (DNA-PKcs
 DE Interacting protein) (Kinase interacting protein) (KIP) (CIB).
 GN CIB1 OR PRKDCIP OR KIP OR CIB.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID-10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-99452760; PubMed-10523297;
 RA Kauselmann G., Weller M., Wulff P., Jessberger S., Konietzko U.,
 RA Scafidi J., Staubli U., Bereliter-Hahn J., Strehhardt R., Kuhl D.;
 RT "The polo-like protein kinases Fnk and Snk associate with a Ca(2+)-and
 RT integrin-binding protein and are regulated dynamically with synaptic
 RT plasticity.";
 RL EMBO J. 18:5528-5539(1999).

CC -1- FUNCTION: MAY CONVERT THE INACTIVE CONFORMATION OF INTEGRIN ALPHA-
 CC IIB/BETA3 TO AN ACTIVE FORM THROUGH THE BINDING TO THE INTEGRIN
 CC CYTOPLASMIC DOMAIN (BY SIMILARITY).
 CC -1- SUBUNIT: INTERACTS WITH THE HETERODIMERIC INTEGRIN ALPHA-
 CC IIB/BETA3. INTERACTS WITH THE PROTEIN KINASES SNK AND WITH THE
 CC REGION IMMEDIATELY UPSTREAM OF THE KINASE DOMAIN OF DNA-PK (BY
 CC SIMILARITY).
 CC -1- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
 CC -----
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DR EMBL; AF136585; AAF08368.1; -
 DR HSSP; Q99828; 1DGV.
 DR InterPro; IPR002048; EF-hand.
 DR Pfam; PF00036; ehand; 2.
 DR Prodom; PD000012; EF-hand; 1.

DR SMART; SM00054; EFh; 2.
 DR PROSITE; PS00018; EF_HAND; 2.
 KW Calcium-binding; Repeat.
 FT CA_BIND 116 127 EF-HAND 1 (POTENTIAL).
 FT CA_BIND 161 172 EF-HAND 2 (POTENTIAL).
 SO SEQUENCE 191 AA; 21800 MW; 3B00B0228679FCC7 CRC64;

Query Match 94.6%; Score 855; DB 1; Length 191;
 Best Local Similarity 88.0%; Pred. NO. 9.2e-58;
 Matches 168; Conservative 15; Mismatches 8; Indels 0; Gaps 0;

QY 1 MGSGSRLSKELLAEXODLTLTKOEILAHRRFCCLLPQEQRTVESSLRAQVPEQILS 60
 DB 1 MGSGSRLSKELLAEXODLTLTKOEILAHRRFCCLLPQEQRTVESSLRAQVPEQILS 60
 QY 61 LPELKANPFEKRICRVSTSPAKDSLSFEDFLDLVSFSDTATPDIKSHYAFRIFFXXXXX 120
 DB 61 LPELKANPFEKRICRVSTSPAKDSLSFEDFLDLVSFSDTATPDIKSHYAFRIFFDDDD 120
 QY 121 XXXXXXXXSRVNCNLTGEGEDTRLASASEMKQIDNILEESDIDRDGTINLSEFQHVISRS 180
 DB 121 GTLDREDSLRLVNCNLTGEGEDTRLASASEMKQIDNILEESDIDRDGTINLSEFQHVISRS 180
 QY 181 PDFASSFKIVL 191
 DB 181 PDFASSFKIVL 191

RESULT 4

KIP2_MOUSE
 ID KIP2_MOUSE STANDARD; PRT; 187 AA.
 AC Q9Z309;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Kinase interacting protein 2 (KIP 2).
 GN KIP2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID-10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Brain, and Testis;
 RX MEDLINE-99132027; PubMed-9931475;
 RA Sekl N., Hattori A., Hayashi A., Kozuma S., Ohlra M., Horl T.,
 RA Salto T.;
 RT "Structure, expression profile and chromosomal location of an isoform
 RT of DNA-PKcs interacting protein (KIP) gene.";
 RL Blochim. Biophys. Acta 1444:143-147(1999).

CC -1- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
 CC -----
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DR EMBL; AB016080; BAA36545.1; -
 DR HSSP; Q99828; 1DGV.
 DR MGI; MGI:1929293; KIP2.
 DR InterPro; IPR002048; EF-hand.
 DR Pfam; PF00036; ehand; 3.
 DR Prodom; PD000012; EF-hand; 1.
 DR SMART; SM00054; EFh; 2.
 DR PROSITE; PS00018; EF_HAND; 2.
 KW Calcium-binding; Repeat.
 FT CA_BIND 116 127 EF-HAND 1 (POTENTIAL).
 FT CA_BIND 157 168 EF-HAND 2 (POTENTIAL).
 SO SEQUENCE 187 AA; 21703 MW; D21D21DCBD0B6F5C CRC64;

RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Sviderskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of *Drosophila melanogaster*.";
RL Science 287:2185-2195(2000).
CC -1- FUNCTION: CALCINEURIN IS A CALCIUM BINDING AND CALMODULIN BINDING
CC PROTEIN FOUND IN ALL CELLS FROM YEAST TO MAMMALS, IT IS A CALCIUM
CC DEPENDENT, CALMODULIN STIMULATED PROTEIN PHOSPHATASE (BY
CC SIMILARITY).
CC -1- SUBUNIT: COMPOSED OF TWO COMPONENTS (A AND B), THE A COMPONENT IS
CC THE CATALYTIC SUBUNIT AND THE B COMPONENT CONFERS CALCIUM
CC SENSITIVITY (BY SIMILARITY).
CC -1- MISCELLANEOUS: THIS PROTEIN HAS FOUR FUNCTIONAL CALCIUM-BINDING
CC SITES.
CC -1- SIMILARITY: TO OTHER EF-HAND CALCIUM BINDING PROTEINS.
CC -1- CAUTION: Ref.2 sequence differs from that shown due to erroneous
CC gene model prediction.
CC -----
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CC -----
DR EMBL; U56245; AAC47350.1; .
DR EMBL; AE003840; AAF59195.1; ALT_SEQ.
DR HSSP; P06705; 1TCO.
DR FlyBase; FBgn0015614; CanB2.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR001125; Recoverin.
DR Pfam; PF00036; ehand; 4.
DR PRINTS; PR00450; RECOVERIN.
DR ProDom; PD000012; EF-hand; 2.
DR SMART; SM00054; EFh; 4.
DR PROSITE; PS00018; EF_HAND; 4.
DR Kew
KW Calcium-binding; Repeat.
FT CA_BIND 31 42 EF-HAND 1 (POTENTIAL).
FT CA_BIND 63 74 EF-HAND 2 (POTENTIAL).
FT CA_BIND 100 111 EF-HAND 3 (POTENTIAL).
FT CA_BIND 141 152 EF-HAND 4 (POTENTIAL).
SQ SEQUENCE 170 AA; 19267 MW; FDB1BD9DB5A4BDEC CRC64;

Query Match 17.9%; Score 161.5; DB 1; Length 170;
Best Local Similarity 21.9%; Pred. No. 3.1e-05;
Matches 39; Conservative 52; Mismatches 68; Indels 19; Gaps 4;

OY 3 GSGSRSLKELLAEYQDLFTLTKQELLAHRRFCELLPQEQRTVESSLRAQVPEQILSLP 62
Db 2 GNETSLEPMWCNSNFD-----ADEIRRLGKRF-----RKLDIDNSGALSDVEFMSLP 47

OY 63 ELKANPEKERICRVFTSPAKDSIFEDELDSLVSFSDTATPDIKSHYAFRIEXXXXXX 122
Db 48 ELQONPLVQRVIDIFD-ADGNGEYDFKEFIQGSQSVKGDLSKLRAFRIRYDMNDGY 106

OY 123 XXXXXXSRLVNLGTGEGDTRLSASEMKQLIDNILESDIDRDGTLNLSFQHVISRS 180
Db 107 ISNGELFQVLKMGV-----NNLKDITQLQIVDKTIGFADKDEGKISDFEFCVVGNT 160

RESULT 13
CA22_MOUSE STANDARD; PRT; 194 AA.
AC Q62877;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Calcium-binding protein p22 (Calcium-binding protein CHP) (Calcineurin

DE homologous protein) (S1d470).
GN CHP.
OS Mus musculus (Mouse), and
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090, 10116;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES-Rat; TISSUE-Liver;
RX MEDLINE=96215311; PubMed=8626580;
RA Barroso M.R., Bernd R.K., Dewitt N.D., Chang A., Mills K.,
RA Sztul E.S.;
RT "A novel Ca2+-binding protein, p22, is required for constitutive
RT membrane traffic.";
RL J. Biol. Chem. 271:10183-10187(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES-Rat; TISSUE-Brain;
RX MEDLINE=21374135; PubMed=11481038;
RA Matsumoto M., Miyake Y., Nagita M., Inoue H., Shitakubo D.,
RA Takemoto K., Ohtsuka C., Murakami H., Nakamura N., Kanazawa H.;
RT "A serine/threonine kinase which causes apoptosis-like cell death
RT interacts with a calcineurin B-like protein capable of binding Na+/H+
RT exchanger.";
RL J. Biochem. 130:217-225(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES-Mouse;
RA Seki N., Hattori A., Hayashi A., Kozuma S., Muramatsu M., Salto T.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC SPECIES-Mouse; STRAIN=C57BL/6J; TISSUE-Liver;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Salto R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Glass C., Kling B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamlya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weltz C., Whitaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
CC -1- FUNCTION: REQUIRED FOR CONSTITUTIVE MEMBRANE TRAFFIC.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- TISSUE SPECIFICITY: Ubiquitously expressed.
CC -1- PTM: BOTH N-MYRISTOYLATION AND CALCIUM-MEDIATED CONFORMATIONAL
CC CHANGES ARE ESSENTIAL FOR ITS FUNCTION.
CC -1- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
CC -----
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CC -----
DR EMBL; U39875; AAB04146.1; .
DR EMBL; AB070350; BAB63369.1; .
DR EMBL; AB025217; BAA84688.1; .

```
DR EMBL; AK005067; BAB23791.1; -.
DR HSSP; P06705; 1AUI.
DR MGD; MGI:1927185; Chp.
DR InterPro; IPR002048; EF-hand.
DR Pfam; PF00036; ehand; 3.
DR ProDom; PD000012; EF-hand; 2.
DR SMART; SM00054; EFh; 2.
DR PROSITE; PS00018; EF_HAND; 1.
KW Calcium-binding; Repeat; Myristate.
FT INIT_MET 0 0
FT LIPID 1 1 MYRISTATE (PROBABLE).
FT DOMAIN 38 49 ANCESTRAL CALCIUM SITE 1 (POTENTIAL).
FT DOMAIN 70 81 ANCESTRAL CALCIUM SITE 2 (POTENTIAL).
FT CA_BIND 122 133 EF-HAND 3 (BY SIMILARITY).
FT CA_BIND 163 174 EF-HAND 4 (BY SIMILARITY).
FT MUTAGEN 133 133 *E->A: LOSS OF TARGETING/FUSION FUNCTION.
SQ SEQUENCE 194 AA; 22301 MW; E2DF3E5F627B8231 CRC64;

Query Match 17.7%; Score 160; DB 1; Length 194;
Best Local Similarity 24.2%; Pred. No. 5e-05;
Matches 47; Conservative 44; Mismatches 71; Indels 32; Gaps 6;

QY 5 GSR----LSKELLAEQDLTLTKQELLAHRRFCCLLPQEQRTVSSLRAQVFEQILS 60
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 GSRATLLRDEELEIKKTEGESHQSQITRLYSRFTSLDKGNGTLRS-----EDFQR 52

QY 61 LPELKANPFKERICRVFSTSPAKDSLSFEDFLDLLSVF-----SDTATPD----- 105
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 53 IPELAINPLGDRRIINAF-FSEGEDQVNFGRGFMRTLAFPRPIEDNEKSKDVNGPEPLNSRS 111

QY 106 IKSHYAFRIFXXXXXXXSRVNLCTGEGEDPRLSASEMKQLIDNILEESIDRD 165
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 112 NKLHFAFRLYDLKDKKISRDELLQVLRMVG----VNISDEQLGSLADRTIQEADQGD 167

QY 166 GTINLSEFQHVISR 179
   | : || | | | :
Db 168 SAISTFEVVKLEK 181

RESULT 14
CALB_DROME STANDARD; PRT; 170 AA.
AC P48451; Q9W4D0;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Calcineurin B subunit, isoform 1 (Protein phosphatase 2B regulatory
DE subunit).
GN CANB OR CANB1 OR CNB1 OR CNB OR CG4209.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93054551; PubMed=1331060;
RA Guerini D., Montell C., Klee C.B.;
RT "Molecular cloning and characterization of the genes encoding the two
RT subunits of Drosophila melanogaster calcineurin.";
RL J. Biol. Chem. 267:22542-22549(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celnikier S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Vandal M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
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RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fosler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulo G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpsons M.D., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svrtkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
CC -!- FUNCTION: CALCINEURIN IS A CALCIUM BINDING AND CALMODULIN BINDING
CC PROTEIN FOUND IN ALL CELLS FROM YEAST TO MAMMALS, IT IS A CALCIUM
CC DEPENDENT, CALMODULIN STIMULATED PROTEIN PHOSPHATASE (BY
CC SIMILARITY).
CC -!- SUBUNIT: COMPOSED OF TWO COMPONENTS (A AND B), THE A COMPONENT IS
CC THE CATALYTIC SUBUNIT AND THE B COMPONENT CONFERS CALCIUM
CC SENSITIVITY (BY SIMILARITY).
CC -!- MISCELLANEOUS: THIS PROTEIN HAS FOUR FUNCTIONAL CALCIUM-BINDING
CC SITES.
CC -!- SIMILARITY: TO OTHER EF-HAND CALCIUM BINDING PROTEINS.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M97215; AAA28411.1; -.
CC EMBL; AE003434; AAF46026.1; -.
CC HSSP; P06705; ITCO.
CC FlyBase; FBgn0010014; CanB.
CC InterPro; IPR002048; EF-hand.
CC Pfam; PF00036; ehand; 4.
CC ProDom; PD000012; EF-hand; 2.
CC SMART; SM00054; EFh; 4.
CC PROSITE; PS00018; EF_HAND; 4.
KW Calcium-binding; Repeat.
FT CA_BIND 31 42 EF-HAND 1 (POTENTIAL).
FT CA_BIND 63 74 EF-HAND 2 (POTENTIAL).
FT CA_BIND 100 111 EF-HAND 3 (POTENTIAL).
FT CA_BIND 141 152 EF-HAND 4 (POTENTIAL).
SQ SEQUENCE 170 AA; 19341 MW; 77D89BE9BD961900 CRC64;

Query Match 17.4%; Score 157.5; DB 1; Length 170;
Best Local Similarity 23.2%; Pred. No. 6.3e-05;
Matches 36; Conservative 47; Mismatches 59; Indels 13; Gaps 3;

QY 26 ETLAHRRCCELLPQEQRTVSSLRAQVFEQILSLPELKANPFKERICRVFSTSPAKDS 85
   || | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 19 EIRRLGKRF-----RKLDLNSGALSIDFMSLPQLQNPVQRVIDIFD-ADGNGE 69
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OY 86 LSFEDLDLVSFDPATPDIKSHYAFRIEXXXXXXXXXXXXXXXXXXSRVNLCTGEGEDTRL 145
DB 70 VDFKEFIQVSGVSVRGDKLSKLRFAFRIDYDMNDGYSNGELFOVLKMMVG-----NNLK 125
OY 146 ASEMQLIDNILESDIDRDGTINLSEFQHVISR 180
DB 126 DTLOQIVDKTICFADKDEDGKISFDFCSVVGNT 160

RESULT 15
CA22_HUMAN STANDARD; PRT; 194 AA.
AC Q99653;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Calcium-binding protein p22 (Calcium-binding protein CHP) (Calcineurin
DE homologous protein) (Calcineurin B homolog).
GN CHP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=B-cell;
RX MEDLINE=97057295; PubMed=8901634;
RA Lin X., Barber D.L.;
RT "A calcineurin homologous protein inhibits GTPase-stimulated Na-H
RT exchange."
RL Proc. Natl. Acad. Sci. U.S.A. 93:12631-12636(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Muscle;
RA Strausberg R.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: REQUIRED FOR CONSTITUTIVE MEMBRANE TRAFFIC (BY
CC SIMILARITY). INHIBITS GTPASE-STIMULATED NA-H EXCHANGE.
CC SPECIFICALLY BINDS TO THE SODIUM/HYDROGEN EXCHANGER 1 (NHE1) AT A
CC DOMAIN THAT IS CRITICAL FOR GROWTH FACTOR STIMULATION OF EXCHANGE
CC ACTIVITY.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- TISSUE SPECIFICITY: UBIQUITOUSLY EXPRESSED. HAS BEEN FOUND IN
CC FETAL EYE, LUNG, LIVER, MUSCLE, HEART, KIDNEY, THYMUS AND SPLEEN.
CC -!- PTM: BOTH N-MYRISTOYLATION AND CALCIUM-MEDIATED CONFORMATIONAL
CC CHANGES ARE ESSENTIAL FOR ITS FUNCTION IN EXOCYTIC TRAFFIC
CC (BY SIMILARITY).
CC -!- PTM: PHOSPHORYLATED IN VIVO. DECREASE IN ITS PHOSPHORYLATION IS
CC ASSOCIATED WITH AN INCREASE IN EXCHANGE ACTIVITY. THE
CC PHOSPHORYLATION STATE MAY REGULATE THE BINDING TO NHE1.
CC -!- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
CC -----
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U61538; AAB37770.1; -
DR EMBL; BC001646; AAH01646.1; -
DR HSSP; P06705; IAU1.
DR MIM; 606988; -
DR InterPro; IPR002048; EF-hand.
DR Pfam; PF00036; efhand; 3.
DR ProDom; PD000012; EF-hand; 2.
DR SMART; SM00054; EFh; 2.
DR PROSITE; PS00018; EF_HAND; FALSE_NEG.
KW Calcium-binding; Repeat; Myristate; Phosphorylation.
FT INIT_MET 0
FT LIPID 1
FT DOMAIN 38 49 ANCESTRAL CALCIUM SITE 1 (POTENTIAL).

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FT DOMAIN 70 81 ANCESTRAL CALCIUM SITE 2 (POTENTIAL).
FT CA_BIND 122 133 EF-HAND 3 (BY SIMILARITY).
FT CA_BIND 163 174 EF-HAND 4 (BY SIMILARITY).
SQ SEQUENCE 194 AA; 22325 MW; 17DDEE5F03C88380 CRC64;

Query Match 17.3%; Score 156; DB 1; Length 194;
Best Local Similarity 23.7%; Pred. No. 0.0001;
Matches 46; Conservative 44; Mismatches 72; Indels 32; Gaps 6;

OY 5 GSR----LSKELLAEXODLFTLTKOEILLAHRRFCCLLPQEQRTVSSLRQVFEQILS 60
DB 1 GSRASFLLRDEELEIKETGFSHSQITRLYSRFTSLDKENGTLR-----EDFOR 52
OY 61 LPELKANPFKERICRVFSTSPAKDSLSFEDFLDLVSF-----SDPATPD----- 105
DB 53 IPELAINPLGDRINAFPE-GEQVNFGRFMRLAHRPIEDNEKSKDVNGPEPLNSRS 111
OY 106 IKSHYAFRIEXXXXXXXXXXXXXXXXXXSRVNLCTGEGEDTRLASASEMQLIDNILESDIDRD 165
DB 112 NKLHFAFRLYDLDKDKISRDELLQVLRMMVG-----VNISDEQLGSIADRTIQEADQDGD 167
OY 166 GTINLSEFQHVISR 179
DB 168 SAISFTEFVKYLEK 181

```

Search completed: January 17, 2003, 12:51:16
Job time : 14 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 17, 2003, 12:49:40 ; Search time 31 Seconds

(Without alignments)
1269.516 Million cell updates/sec

Title: US-09-878-454A-2X

Perfect score: 904
Sequence: 1 MGGSGSRSLSKELLAERYODLT.....EFQHVISRSPDFASSFKIVL.191

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 671580 segs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPRREMBL_21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriaph:*
17: sp_archaeap:*

Pred. NO. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	393	43.5	311	5	Q93640	Q93640 caenorhabdi
2	344	38.1	185	11	Q9D9N5	Q9D9N5 mus musculu
3	337	37.3	187	4	Q96Q77	Q96Q77 homo sapien
4	320.5	35.5	206	5	Q9W2Q5	Q9W2Q5 drosophila
5	219	24.2	54	6	Q9G1J2	Q9G1J2 sus scrofa
6	214.5	23.7	180	5	Q9GP83	Q9GP83 dictyostell
7	186	20.6	175	10	Q93VF2	Q93VF2 eucalyptus
8	186	20.6	175	10	Q9LS47	Q9LS47 arabidopsis
9	184	20.4	175	5	Q9U0X7	Q9U0X7 leishmania
10	169.5	18.8	169	5	Q9NFN1	Q9NFN1 schistosoma
11	169.5	18.8	244	5	Q20804	Q20804 caenorhabdi
12	165.5	18.3	170	5	Q9NKM7	Q9NKM7 patinopecte
13	165.5	18.3	195	5	Q23643	Q23643 caenorhabdi
14	164.5	18.2	213	5	Q16343	Q16343 caenorhabdi
15	163.5	18.1	170	5	Q95P81	Q95P81 bombyx mori
16	163	18.0	200	5	Q8SRF8	Q8SRF8 encephalito

17	162.5	18.0	115	11	Q99LQ9	Q99LQ9 mus musculu
18	162	17.9	274	10	Q9AMW4	Q9AMW4 oryza sativ
19	159.5	17.6	213	10	Q9LTB8	Q9LTB8 arabidopsis
20	157.5	17.4	175	3	Q9HDE1	Q9HDE1 cryptococcu
21	157.5	17.4	177	3	Q9HDD3	Q9HDD3 cryptococcu
22	156.5	17.3	226	10	Q81446	Q81446 arabidopsis
23	155	17.1	170	4	Q8WYJ4	Q8WYJ4 homo sapien
24	155	17.1	173	4	Q96LZ3	Q96LZ3 homo sapien
25	151.5	16.8	161	10	Q9AY39	Q9AY39 oryza sativ
26	151.5	16.8	187	5	Q9VWX8	Q9VWX8 drosophila
27	149.5	16.5	189	5	Q9VNF9	Q9VNF9 drosophila
28	146	16.2	192	10	Q81328	Q81328 arabidopsis
29	146	16.2	225	10	Q8W5C8	Q8W5C8 oryza sativ
30	144.5	16.0	226	10	Q81447	Q81447 arabidopsis
31	143	15.8	190	3	Q96X50	Q96X50 magnaporthe
32	143	15.8	190	3	Q8TGC0	Q8TGC0 magnaporthe
33	142	15.7	196	5	Q9N2Y1	Q9N2Y1 caenorhabdi
34	142	15.7	246	10	Q82641	Q82641 arabidopsis
35	140.5	15.5	213	10	Q81445	Q81445 arabidopsis
36	140	15.5	29	11	Q99JY5	Q99JY5 mus musculu
37	138	15.3	190	5	Q9NAY9	Q9NAY9 naegleria f
38	137	15.2	214	10	Q9FUQ7	Q9FUQ7 arabidopsis
39	137	15.2	214	11	Q8VCN1	Q8VCN1 mus musculu
40	137	15.2	224	10	Q9SGW7	Q9SGW7 arabidopsis
41	136	15.0	222	10	Q81223	Q81223 arabidopsis
42	134.5	14.9	153	5	Q9U5J0	Q9U5J0 trichomonas
43	134.5	14.9	160	5	Q9U5I9	Q9U5I9 trichomonas
44	131	14.5	216	4	Q9NWT9	Q9NWT9 homo sapien
45	129	14.3	191	4	Q9UM19	Q9UM19 homo sapien

ALIGNMENTS

RESULT 1

Q93640 ID Q93640 PRELIMINARY; PRT; 311 AA.
AC Q93640; 01-FEB-1997 (TREMBlrel. 02, Created)
DT 01-FEB-1997 (TREMBlrel. 02, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE F30A10.1 protein.
GN F30A10.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN (1)
RP SEQUENCE FROM N.A.
RA Barlow K.;
RL Submitted (OCF-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE-99069613; PubMed-9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
investigating biology.";
RL Science 282:2012-2018(1998).
DR EMBL; Z81072; CAB03019.1; .
DR HSSP; Q99828; IDGV.
DR InterPro; IPR002048; EF-hand.
DR Pfam; PF00036; efhand; 3.
DR ProDom; PD00012; EF-hand; 1.
DR SMART; SM00054; EFh; 2.
SO SEQUENCE 311 AA; 35960 MW; 97AF0AF56A6F526F CRC64;

Query Match 43.5%; Score 393; DB 5; Length 311;
Best Local Similarity 39.6%; Pred.No. 4.1e-24;
Matches 82; Conservative 52; Mismatches 47; Indels 26; Gaps 5;
QY 1 MGGSGSRSLSKELLAERYODLTFLTKQELLAHRRFCCELLPQEQRYESS 48
DB 111 MGNMSSISSELNLFSGGVFTREQDDEYQDCTFTTRKDIIRLYKRYALNPHK---VPTN 167

RC STRAIN-BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazey R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayanti A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Bailew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrera S., Fleischmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,
RA Jaitai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svitskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of *Drosophila melanogaster*.";
RL Science 287:2185-2195(2000).
DR EMBL; AE003452; AAF46635.1; -.
DR HSSP; Q99828; 1DGV.
DR FlyBase; FBgn0034558; CG9236.
DR InterPro; IPR002048; EF-hand.
DR Pfam; PF00036; efhand; 3.
DR ProDom; PD000012; EF-hand; 1.
DR SMART; SM00054; EFh; 3.
DR PROSITE; PS00018; EF_HAND; 2.
KW Calcium-binding.
SQ SEQUENCE 206 AA; 23591 MW; B3105F7E70F475A9 CRC64;

	Query Match	35.5%;	Score 320.5;	DB 5;	length 206;
	Best Local Similarity	40.98;	Pred. No. 2.2e-18;		
	Matches 72;	Conservative 41;	Mismatches 46;	Indels 17;	Gaps 5;
QY	17 QDLFLTKQEILLAHRRFCCLLPQ--EQRTVESSLRAYVPFEQILSLPELKANPFKERI	73			
Dd	43 KDCTFFTRKEILRVHKRRELRPDLVPRöMTEGQASSVKVPCCECIEMPELR-----	94			
QY	74 CRVFSTSPAKDSLSEDFLDLLSVFSDTATPDIKSHYAERIFXXXXXXXSRLVN	133			
Dd	95 -EAFSRD-GQGNTLSEFDLDALSVFSEQAPRDIKVFAYEKTYDDQDGFIGHAD---LMS	149			
QY	134 CLTGEGEDTRLASSEMQLIDNILEESDIDRDGTINLSEFOHVISRSPDFASSFKI	189			
Dd	150 CLTTMTKN-ELSPEEHQIADKVIIEADVGDGKLSTLEFEHVILRAPDFLSTFHl	204			
RESULT	5				
Q9GLJ2					
ID	Q9GLJ2	PRELIMINARY;	PRT;	54 AA.	
AC	Q9GLJ2;				
DT	01-MAR-2001 (Tremblrel, 16, Created)				

```

DT 01-MAR-2001 (TREMBLrel. 16, last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, last annotation update)
DE DNA-PK interaction-like protein (Fragment).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Smith T.P.L., Fahrenkrug S.C., Rohrer G.A., Slimmen F.A.,
RA Rexroad C.E. III, Keele J.W.;
RT "Mapping of Expressed Sequence Tags from a porcine early embryonic
RT cDNA library.";
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF267715; AAC25931.1; -.
DR HSSP; Q99828; 1DGV.
DR InterPro; IPR002048; EF-hand.
DR Pfam; PF00036; ehand; 1.
DR ProDom; PD000012; EF-hand; 1.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
FT NON_TER 1
FT NON_TER 54
SQ SEQUENCE 54 AA; 6107 MW; 1A8057DE68A57A4A CRC64;

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Query Match      24.2%; Score 219; DB 6; Length 54;
Best Local Similarity 74.1%; Pred. No. 7.5e-11;
Matches 40; Conservative 14; Mismatches 0; Indels 0; Gaps 0;

QY 102 ATPDIKSHYAFRIxxxxxxxsrLVNCLTGEGEDTRLASSEMkOLIDN 155
|||||.....:|||||
Db 1 ATPDIKSHYAFRIEDDDGTLNREDLSQLVNCLTGEGEDTRLASSEMkOLIDN 54

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RESULT 6
Q9GPF83
ID Q9GPF83 PRELIMINARY; PRT; 180 AA.
AC Q9GPF83;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Calcineurin B.
GN CNBA.
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-AX-2;
RA Alchem A.;
RL Thesis (2000), Department of Fachbereich Biologie,
  Universitaet Konstanz, Konstanz, Germany.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-AX-2;
RA Alchem A.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AJ301668; CAC20026.2; -.
DR HSSP; P06705; 1AUT.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR001125; Recoverin.
DR Pfam; PF00036; efhand; 4.
DR PRINTS; PR00450; RECOVERIN.
DR ProDom; PD000012; EF-hand; 2.
DR SMART; SM00054; EFh; 4.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_3.
SQ SEQUENCE 180 AA; 20739 MW; E2E947E8D280D0B6 CRC64;

```

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Query Match      23.7%; Score 214.5; DB 5; Length 180;  
Best Local Similarity 27.0%; Pred. No. 1.1e-09;  
Matches 48; Conservative 54; Mismatches 61; Indels 15; Gaps 4;  
  
QY    1 MGSGSRLSKELLAEYQDITFLTKQEILLAHRRFCCLLPQEQRTVESSLRAQVPFEQLLS 60  
|| |::| | : :: || : || | |
```


Db 1 MGNHSLNKEQLEQKDNSSFSEAEKLYRRFQMLDKDGGTLTT-----DEFLS 52

QY 61 LPELKANPFKERICRVFSTSPAKDS-LSFEFELDLLSVFSDTATPDIKSHYAFRIFXXXX 119

Db 53 IPDLALNPLLERVQIFDQ--KDNEIEFSEFVGTATLSHGKTKEDKLKFLFIYDIDC 110

QY 120 XXXXXXXXSRVLNCLTGEGETRLSASEMKQLIDNILEESDIDRDGTINLSEFQHV 177

Db 111 DGFISNGELFQVLKXMGV---TNLNDVQLQIVDKTIEGDDYDKGKISFDEFIHM 164

RESULT 7

Q93VF2

ID Q93VF2 PRELIMINARY; PRT; 175 AA.

AC Q93VF2;

DT 01-DEC-2001 (Tremblrel. 19, Created)

DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)

DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)

DE Calcineurin-like protein.

GN ECCBL1 OR EGCBL1.

OS Eucalyptus camaldulensis (Murray red gum), and

OS Eucalyptus grandis.

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC eurosids II; Myrtales; Myrtaceae; Eucalyptus.

OX NCBI_TaxID=34316, 71139;

RN [1]

RP SEQUENCE FROM N.A.

RC SPECIES=E.camaldulensis, and E.grandis; TISSUE=FLOWER;

RA Fairbairn D.J., Gomez-Gallego S., Sawbridge T., Teasdale R.D.;

RL Submitted (Oct-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF197334; AAL25650.1; -.

DR EMBL; AF197330; AAL25647.1; -.

DR InterPro; IPR002048; EF-hand.

DR Pfam; PF00036; ehand; 2.

DR ProDom; PD000012; EF-hand; 1.

DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.

SQ SEQUENCE 175 AA; 19997 MW; C4E773EE42A3EF16 CRC64;

Query Match 20.6%; Score 186; DB 10; Length 175;

Best Local Similarity 24.2%; Pred. No. 2.5e-07;

Matches 44; Conservative 54; Mismatches 64; Indels 20; Gaps 4;

QY 1 MGGSGSRLSKELLAEQD--LTFLTKQEILLAHRRFCELLPQEQRVLESSLRAQVPFEQI 58

Db 1 MGNASSMLTQYDIEEVQDHNNLFSQEQEIVSLYERFCQL-----DRNAKGFISADEF 52

QY 59 LSLPELKANPFKERICRVFSTSPAKDSLSFEFELDLLSVFSDTATPDIKSHYAFRIFXXX 118

Db 53 LSVPEFAMNPLSQRLKMW-----DGLNFKDFVAFLSAFSAKASKQKIELIFKVIDSD 106

QY 119 XXXXXXXXSRVLNCLTGEGETRLSASEMKQLIDNILEESDIDRDGTINLSEFQHV 178

Db 107 CNGKVSFNDILEVLRDLG----PFMSDEQREQVLVQVLKEAGYTRSYLLLLDDFKVFG 162

QY 179 RS 180

Db 163 NS 164

RESULT 8

Q9LS47

ID Q9LS47 PRELIMINARY; PRT; 175 AA.

AC Q9LS47;

DT 01-OCT-2000 (Tremblrel. 15, Created)

DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)

DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)

DE Calcineurin b subunit (Protein phosphatase 2b regulatory subunit)-like

DE protein (Hypothetical 20.0 kDa protein).

GN AT3GI8430.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.

OX NCBI_TaxID=3702;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=COLUMBIA;

RA Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata S.;

RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=COLUMBIA;

RX MEDLINE=20277480; PubMed=10819329;

RA Nakamura Y.;

RT "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence

RT features of the regions of 4,504,864 bp covered by sixty P1 and TAC

RT clones.";

RL DNA Res. 7:131-135(2000).

RN [3]

RP SEQUENCE FROM N.A.

RA Yamada K., Banh J., Banno F., Chang E., Dale J.M., Goldsmith A.D.,

RA Lee J.M., Onodera C.S., Quach H.L., Tang C., Toriumi M., Wu H.C.,

RA Yamamura Y., Yu G., Yu S., Bowser L., Carninci P., Chen H., Cheuk R.,

RA Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,

RA Kawai J., Kim C., Koesema E., Lam B., Lin J., Meyers M.C., Miranda M.,

RA Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M.,

RA Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,

RA Theologis A.;

RT "Full length cDNA of gene At3gl8430 (GI:15229640).";

RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.

RN [4]

RP SEQUENCE FROM N.A.

RA Yamada K., Banh J., Chan M.M., Chang C.H., Chang E., Dale J.M.,

RA Deng J.M., Goldsmith A.D., Lee J.M., Onodera C.S., Quach H.L.,

RA Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bowser L.,

RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,

RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,

RA Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J.,

RA Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Shinozaki K.,

RA Davis R.W., Ecker J.R., Theologis A.;

RT "Arabidopsis Open Reading Frame (ORF) Clones.";

RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AB026658; BAB01109.1; -.

DR EMBL; AY063789; AAL36096.1; -.

DR EMBL; AY091287; AAM14226.1; -.

DR HSSP; P06705; LAUI.

DR InterPro; IPR002048; EF-hand.

DR Pfam; PF00036; ehand; 2.

DR ProDom; PD000012; EF-hand; 1.

DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.

KW Hypothetical protein.

SQ SEQUENCE 175 AA; 20032 MW; B26D6F2ADA26AFED CRC64;

Query Match 20.6%; Score 186; DB 10; Length 175;

Best Local Similarity 25.0%; Pred. No. 2.5e-07;

Matches 46; Conservative 53; Mismatches 61; Indels 24; Gaps 5;

QY 1 MGGSGSRLSKELLAEQD--LTFLTKQEILLAHRRFCELLPQEQRVLESSLRAQVPFE 56

Db 1 MGNASSMLTQYDIEEVQSHCHDL--FEQOEILSLYQRFQCL-----DRNAKGFISAD 50

QY 57 QILSLPELKANPFKERICRVFSTSPAKDSLSFEFELDLLSVFSDTATPDIKSHYAFRIFX 116

Db 51 EFLSVPEFAMNPLSQRLKMW-----DGLNFKDFVAFLSAFSAKASLRQKVLIFKVID 104

QY 117 XXXXXXXXSRVLNCLTGEGETRLSASEMKQLIDNILEESDIDRDGTINLSEFQHV 176

Db 105 SDCNGKVSFKDIMEVLRDLG----SFMSDEQREQVLVQVLKESGYTSDSFLTFLEDFIKI 160

QY 177 ISRS 180

Db 161 FGSS 164

RESULT 9

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Q9U0X7
ID Q9U0X7 PRELIMINARY; PRT; 175 AA.
AC Q9U0X7;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, last annotation update)
DE Calcineurin subunit.
GN L7171.06.
OS Leishmania major.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID=5664;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FRIEDLIN;
RA Tosato V., Bruschl C.V., Ivens A.C., Murphy L., Quall M.,
RA Rajandream M.A., Barrell B.G.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FRIEDLIN;
RX MEDLINE=98146435; PubMed=9477341;
RA Ivens A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M.,
RA Smith D.F.;
RT "A physical map of the Leishmania major Friedlin genome.";
RL Genome Res. 8:135-145(1998).
DR EMBL; AL13435; CAB62809.1; -.
DR HSSP; P06705; 1AUI.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR001125; Recoverin.
DR Pfam; PF00036; efhand; 4.
DR PRINTS; PR00450; RECOVERIN.
DR ProDom; PD000012; EF-hand; 2.
DR SMART; SM00054; EFh; 3.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_2.
SQ SEQUENCE 175 AA; 19660 MW; 9448F127FADFA0EB CRC64;
```

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Query Match 20.4%; Score 184; DB 5; Length 175;
Best Local Similarity 22.5%; Pred. No. 3.6e-07;
Matches 41; Conservative 54; Mismatches 73; Indels 14; Gaps 4;
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```
QY 8 LSKELLAERYQDLTFELTKOEILLAHRRFCCELLPQEQRTVESSLRAQVPFEQILSLPELKAN 67
Db 6 LTAELQNIRESSTALTDQVQRLYKSFSL-----NKDKSGKITRAEFNSIPALASN 57
QY 68 PEKERICRVSTSPAKDSLSFEFDLDSVFSSTATPDIKSHYAFRIFXKXXXXXXXXXXXX 127
Db 58 PLVDRVLAVMDTD-GDSTVDFGDFVRALAVLSATSKEDKLRFTFKMYDVGDRISNKD 116
QY 128 XSRLVNCITGEGEDTRLASSEMQLIDNILESDIDRDGTINLSEFOHVISRSPDPASSF 187
Db 117 LFQMLSIMVG---VNLQMQLOQIVDKTFIEADYDRDGYITFEFQ-ALAVNSDFGDR 171
QY 188 KI 189
Db 172 NL 173
RESULT 10
Q9NFNI PRELIMINARY; PRT; 169 AA.
AC Q9NFNI;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, last annotation update)
DE Calcineurin B.
OS Schistosoma mansoni (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigoidida;
OC Schistosomatoidea; Schistosomatidae; Schistosoma.
OX NCBI_TaxID=6183;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20520966; PubMed=11071287;
RA Mecozzi B., Rossi A., Lazzaletti P., Kady M., Kaiser S., Valle C.,
```

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RA C1011 D., Klinkert M.Q.;
RT "Molecular cloning of Schistosoma mansoni calcineurin subunits and
RT Immunolocalization to the excretory system.";
RL Mol. Biochem. Parasitol. 110:333-343(2000).
DR EMBL; AJ276885; CAB93677.1; -.
DR HSSP; P06705; 1TCO.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR001125; Recoverin.
DR Pfam; PF00036; efhand; 4.
DR PRINTS; PR00450; RECOVERIN.
DR ProDom; PD000012; EF-hand; 2.
DR SMART; SM00054; EFh; 4.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_4.
SQ SEQUENCE 169 AA; 19137 MW; 878E01D08BC5DC1D CRC64;
```

```
Query Match 18.8%; Score 169.5; DB 5; Length 169;
Best Local Similarity 26.0%; Pred. No. 5.4e-06;
Matches 32; Conservative 42; Mismatches 44; Indels 5; Gaps 2;
```

```
QY 56 EQILSLPELKANPEKERICRVSTSPAKDSLSFEFDLDSVFSSTATPDIKSHYAFRI 115
Db 40 KEFMSLPQLQNPLVARVIEIRPTD-GNGEVDKFEFINGMQFSAKGEAKLKFAFKIY 98
QY 116 XXXXXXXXXXXXSRLVNCITGEGEDTRLASSEMQLIDNILESDIDRDGTINLSEFQH 175
Db 99 DMDKDGYSNGELFQVLMKMWG---NNLKDTQLQIQVKTIMFPDKDEDDGRISFEERCE 154
QY 176 VIS 178
Db 155 VVS 157
```

RESULT 11

```
Q20804 PRELIMINARY; PRT; 244 AA.
AC Q20804;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, last annotation update)
DE F55C10.1 protein.
GN F55C10.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabdiltida; Rhabditoidea;
OC Rhabdiltidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Dobson R.;
RL submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
RT Investigating biology.";
RL Science 282:2012-2018(1998).
DR EMBL; Z74036; CAA98489.2; -.
DR HSSP; P06705; 1AUI.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR001125; Recoverin.
DR Pfam; PF00036; efhand; 4.
DR PRINTS; PR00450; RECOVERIN.
DR ProDom; PD000012; EF-hand; 2.
DR SMART; SM00054; EFh; 4.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_4.
SQ SEQUENCE 244 AA; 27901 MW; 6B99CB58CB77D08B CRC64;
```

```
QY 3 GSGSRLSKELLAERYO-DLTFELTKOEILLAHRRFCCELLPQEQRTVESSLRAQVPFEQILS 60
Query Match 18.8%; Score 169.5; DB 5; Length 244;
Best Local Similarity 25.0%; Pred. No. 9.5e-06;
Matches 45; Conservative 48; Mismatches 64; Indels 23; Gaps 6;
```

Db 75 GADASLPMEMCSNFDAYELRLT-----RRFKL-----DVDGS--GSLSVFEFMS 118

QY 61 LPELKANPFKERICRVFSTSPAKDSLSFEDFLDLSVFSDTATPDIKSHYAFRIFXXXXX 120

Db 119 LPELQNPVQVRVIDFD-EDNGEVDFREFTQGISQFSVKGDKNTKLFKFAFIYDMRD 177

QY 121 XXXXXXSRLVNLCTGEGEDTRLSASEMKQLIDNILEESDIDRDGTINLSEFQHVIRS 180

Db 178 GFISNGELFQVLKMMVG-----NNLKDSQLQOIIVDKTILFHKDGDGKISFQEFCDVVEHT 233

RESULT 12

Q9NKW7

ID Q9NKW7 PRELIMINARY; PRT; 170 AA.

AC Q9NKW7;

DT 01-OCT-2000 (TREMBlrel. 15, Created)

DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)

DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)

DE Calcineurin B.

OS Patinopecten yessoensis (Ezo giant scallop) (Yesso scallop).

OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Pectinoidea;

OC Pectinoidea; Pectinidae; Mizuhopecten.

OX NCBI_TaxID=6573;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE-TESTIS;

RA Uryu M., Nakatomi A., Watanabe M., Hatsuse R., Yazawa M.;

RT "Molecular Cloning of cDNA Encoding Two Subunits of Calcineurin from Scallop Testis: Demonstration of Stage-Specific Expression during Maturation of the Testis";

RL J. Biochem. 0:0-0(2000).

DR EMBL; AB041524; BAA94543.1; -.

DR HSSP; P06705; 1AUI.

DR InterPro; IPR002048; EF-hand.

DR InterPro; IPR001125; Recoverin.

DR Pfam; PF00036; ehand; 4.

DR PRINTS; PR00450; RECOVERIN.

DR ProDom; PD000012; EF-hand; 2.

DR SMART; SM00054; EFh; 4.

DR PROSITE; PS00018; EF_HAND; UNKNOWN_4.

SQ SEQUENCE 170 AA; 19238 MW; 9450322698470F44 CRC64;

Query Match 18.3%; Score 165.5; DB 5; Length 170;

Best Local Similarity 22.3%; Pred. No. 1.2e-05;

Matches 39; Conservative 52; Mismatches 65; Indels 19; Gaps 4;

QY 3 GSGSRLSKELLAQYQDLFTLTKQELLAHRRFCELLPQEQRTVSSSLRAQVPFEQILSLP 62

Db 2 GNENSLPMELCSNFD-----PDEIKRLGKRF-----RKLDLNSGSLSVDFMTLP 47

QY 63 ELKANPFKERICRVFSTSPAKDSLSFEDFLDLSVFSDTATPDIKSHYAFRIFXXXXXX 122

Db 48 ELQONPLVQVRVIDFDTD-GNGEVDFKEFIEGVSVKGDKLSKLFKFAFIYDMDKGY 106

QY 123 XXXXXXSRLVNLCTGEGEDTRLSASEMKQLIDNILEESDIDRDGTINLSEFQHV 177

Db 107 ISNGELFQVLKMMVG-----NNLKDTQLQOIIVDKTIIHADADGDKISFEFCVAV 157

RESULT 13

Q23643

ID Q23643 PRELIMINARY; PRT; 195 AA.

AC Q23643;

DT 01-NOV-1996 (TREMBlrel. 01, Created)

DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)

DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)

DE 2K856.8 protein.

GN 2K856.8.

OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;

OC Rhabditidae; Peloderinae; Caenorhabditis.

OX NCBI_TaxID=6239;

RN [1]

RP SEQUENCE FROM N.A.

RA Lloyd C.R.;

RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=99069613; PubMed=9851916;

RA none;

RT "Genome sequence of the nematode C.elegans: A platform for investigating biology.";

RT Science 282:2012-2018(1998).

RL EMBL; Z70783; CAA94856.1; -.

DR HSSP; P06705; 1AUI.

DR InterPro; IPR002048; EF-hand.

DR Pfam; PF00036; ehand; 3.

DR ProDom; PD000012; EF-hand; 2.

DR SMART; SM00054; EFh; 2.

DR PROSITE; PS00018; EF_HAND; UNKNOWN_2.

SQ SEQUENCE 195 AA; 22670 MW; 9F4FDD6D8BD7BA88 CRC64;

Query Match 18.3%; Score 165.5; DB 5; Length 195;

Best Local Similarity 22.3%; Pred. No. 1.4e-05;

Matches 44; Conservative 53; Mismatches 69; Indels 31; Gaps 6;

QY 1 MGSGSRLSKELLAQYQDLFTLTKQELLAHRRFCELLPQEQRTVSSSLRAQVPFEQIL 59

Db 1 MGNSSSLMLRDEIEEIMSETEFNRNQIVRLSYRFLSLDKKGQGLSR-----DDFL 52

QY 60 SLPELKANPFKERICRVFSTSPA-----KDSLSFEDFLDLSVFSDTATPDIKSH---- 109

Db 53 NVPELAVNPLGDRIVDAFFTLASSNGDNEEQQLNFRQFVRLAHFQPISR--VKKNALNS 110

QY 110 -----YAFRIFXXXXXXXSRLVNLCTGEGEDTRLSASEMKQLIDNILEESDID 163

Db 111 RKDKLLFAFKMYDLNKNNDYITREEFKVILNSMVG-----ANTSDQLDKIADRTIEADAD 166

QY 164 RDGTINLSEFQHVIRS 180

Db 167 RDGKISFEFCRAMET 183

RESULT 14

O16343

ID O16343 PRELIMINARY; PRT; 213 AA.

AC O16343;

DT 01-JAN-1998 (TREMBlrel. 05, Created)

DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)

DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)

DE F59D6.7 protein.

GN F59D6.7.

OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;

OC Rhabditidae; Peloderinae; Caenorhabditis.

OX NCBI_TaxID=6239;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-BRISTOL N2;

RX MEDLINE=94150718; PubMed=7906398;

RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M., Coulson A., Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Fulton L., Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L., Jones M., Kershaw J., Kirsten J., Laister N., Latreille P., Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M., Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R., Smaldon N., Smith A., Sonhammer E., Staden R., Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J., Wohlman P., "2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans.";

RL Nature 368:32-38(1994).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN-BRISTOL N2;

RA Bradshaw H., Graves T.;
RT "The sequence of C. elegans cosmid F59D6."
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
RN (3)
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Waterston R.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF016435; AAB65882.1; -
DR HSSP; P06705; IAU1.
DR InterPro; IPR002048; EF-hand.
DR Pfam; PF00036; efhand; 4.
DR ProDom; PD000012; EF-hand; 2.
DR SMART; SM00054; EFh; 2.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_2.
SQ SEQUENCE 213 AA; 24432 MW; AB19689122E91391 CRC64;

Query Match 18.2%; Score 164.5; DB 5; Length 213;
Best Local Similarity 22.1%; Pred. No. 2e-05;
Matches 47; Conservative 53; Mismatches 68; Indels 45; Gaps 7;

OY 1 MGGSGSRL-----SKELLAEO-----DLTFLTKOEILLAHRRFCCELLPQE 41
Db 1 MGNSNSSILSDAEMREIMDETQCKVCVIAKQFTPKNTISVNHQILRLYTRFASL----- 56
OY 42 QRTVESSLRAQVFEQILSLPELKANPFKERICRVSTSPAKD-----SLSFEDFLDL 95
Db 57 ----DKNGGYLRDDELINPELAVNPLGDRILDAFFTLGSDSDGSKSGQLTFRQFVRIL 112
OY 96 SVF-----SDTATPDIKS--HYAFRIFFXXXXXXXSRVLVNCITGEGEDTRLAS 147
Db 113 AHFOPISKYKDNALNSRKDKLRFAPFKMYDLNNNYITREEFKVILNSMVG----ANITSD 168
OY 148 EMKQIDNILESDIDRDGTINLSEFOHYISRS 180
Db 169 QLDKIADKTELEADQDRDGKISFEDFCRAEMKT 201

RESULT 15

Q95P81 PRELIMINARY; PRT; 170 AA.
ID O95P81;
AC Q95P81;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update).
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Calcineurin B.
GN CNB.
OS Bombyx mori (Silk moth).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Bombycoidea; Bombycidae; Bombyx.
OX NCBI_TaxID=7091;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SHUKO X RYUHAU; TISSUE-PHEROMONE GLAND;
RA Yoshiga T., Matsumoto S.;
RT "cDNA cloning of heterosubunits of calcineurin from pheromone gland of
RT Bombyx mori."
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF287251; AAK83039.1; -
DR InterPro; IPR002048; EF-hand.
DR Pfam; PF00036; efhand; 4.
DR ProDom; PD000012; EF-hand; 2.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_4.
SQ SEQUENCE 170 AA; 19357 MW; 5ECC15B820097130 CRC64;

Query Match 18.1%; Score 163.5; DB 5; Length 170;
Best Local Similarity 21.9%; Pred. No. 1.7e-05;
Matches 39; Conservative 53; Mismatches 67; Indels 19; Gaps 4;

OY 3 GSGSRLSKELLAEODLTFLTKOEILLAHRRFCCELLPQERTVESSLRAQVFPFQILSLP 62
Db 2 GNENSIPMELCSNFD-----ADEIRRLGKRF-----RKLDLDNSGALSIDEFMSLP 47

OY 63 ELKANPEKERICRVSTSPAKDSLSFEDFLDLVSFSDTATPDIKSHYAFRIFFXXXXXX 122
Db 48 ELQONFLVQRVIDIFD-ADGNGEVDKFEFIQGVSOFSVKGDKLSKLRFAFRITDMDNGF 106
OY 123 XXXXXSRVLVNCITGEGEDTRLASSEMKQIDNILESDIDRDGTINLSEFOHYISRS 180
Db 107 ISNGELFQVLRKMGV-----NNLKDTQLQOIYDKTILFADKDEDGKISFEFCNVVGNP 160

Search completed: January 17, 2003, 12:51:54
Job time : 32 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 17, 2003, 12:42:03 ; Search time 13 Seconds

(without alignments)
609.383 Million cell updates/sec

Title: MUT127

Perfect score: 957

Sequence: 1 MGGSGSRLSKELLAAYQDLT.....EFQHVISRSPDFASSFKIVL 191

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	ID	Description
1	955	99.8	191	1	KIP1_HUMAN
2	902	94.3	191	1	KIP1_MOUSE
3	901	94.1	191	1	KIP1_RAT
4	338	35.3	187	1	KIP2_MOUSE
5	336	35.1	187	1	KIP2_HUMAN
6	213.5	22.3	177	1	CALB_NAEGR
7	207.5	21.7	174	1	CALB_SCHPO
8	196.5	20.5	174	1	CALB_NEUCR
9	196.5	20.5	174	1	CALB_YEAST
10	183.5	19.2	169	1	CALB_HUMAN
11	183.5	19.2	169	1	CALB_MOUSE
12	175.5	18.3	170	1	CA22_MOUSE
13	175	18.3	194	1	CA22_MOUSE
14	171.5	17.9	170	1	CALB_DROME
15	170	17.8	194	1	CA22_HUMAN
16	169.5	17.7	178	1	CALC_MOUSE
17	168.5	17.6	186	1	FREQ_DROME
18	167.5	17.5	175	1	CALC_RAT
19	163.5	17.1	189	1	NCS2_CAEEL
20	155	16.2	190	1	APLC_APLCA
21	149.5	15.6	195	1	H520_HUMAN
22	148	15.5	189	1	NCS1_HUMAN
23	148	15.5	189	1	NCS1_XENLA
24	143	14.9	190	1	NCS1_CAEEL
25	143	14.9	192	1	VIS3_CHICK
26	143	14.9	192	1	VIS3_MOUSE
27	142	14.8	192	1	VIS3_HUMAN
28	137	14.3	189	1	NCAH_DROME
29	134	14.0	190	1	VIS2_RAT
30	133.5	13.9	214	1	TESC_HUMAN
31	133	13.9	192	1	NCAD_MOUSE
32	132	13.8	192	1	HIPP_HUMAN
33	128.5	13.4	172	1	CATR_MOUSE

34	128	13.4	192	1	NCAD_CHICK	012953	gallus gall
35	128	13.4	214	1	TESC_MOUSE	091k15	mus musculu
36	127	13.3	192	1	NCAD_HUMAN	P29554	homo saplen
37	127	13.3	192	1	NECX_APLCA	Q16982	homo saplen
38	127	13.3	791	1	KDGG_HUMAN	P49619	homo saplen
39	126	13.2	189	1	NCS1_SCHPO	Q09711	schizosacch
40	125.5	13.1	172	1	CAT2_HUMAN	Q12798	homo saplen
41	125	13.1	190	1	VIS1_HUMAN	P28677	homo saplen
42	125	13.1	804	1	KDGB_HUMAN	Q9y6t7	homo saplen
43	123.5	12.9	195	1	H520_MOUSE	Q9d869	mus musculu
44	121.5	12.7	801	1	KDGB_RAT	P49621	rattus norv
45	121	12.6	189	1	NCS1_YEAST	Q06389	saccharomyc

ALIGNMENTS

RESULT 1
KIP1_HUMAN
ID KIP1_HUMAN STANDARD: PRT; 191 AA.
AC Q99828; 000735; 000693; Q99971; Q96J54;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Calcium and integrin-binding protein 1 (Calmyrin) (DNA-PKcs
DE Interacting protein) (Kinase interacting protein) (KIP) (CIB) (SNK
DE Interacting protein 2-28) (SIP2-28).
GN CIB1 OR PRKDCIP OR KIP OR CIB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Yuan O.;
RT "SNK, a Ser/Thr protein kinase, associated proteins.";
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE-98040126; PubMed-9372844;
RA Wu X., Lieber M.R.;
RT "Interaction between DNA-dependent protein kinase and a novel protein,
RT KIP.";
RL Mutat. Res. 385:13-20(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE-Fetal liver;
RX MEDLINE-97184102; PubMed-9030514;
RA Nalk U.P., Patel P.M., Parise L.V.;
RT "Identification of a novel calcium-binding protein that interacts
RT with the integrin alpha1b cytoplasmic domain.";
RL J. Biol. Chem. 272:4651-4654(1997).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE-20284952; PubMed-10826701;
RA Hattori A., Seki N., Hayashi A., Kozuma S., Saito T.;
RT "Genomic structure of mouse and human genes for DNA-PKcs interacting
RT protein (KIP).";
RL DNA Seq. 10:415-418(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC TISSUE-Cervix;
RA Strausberg R.;
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
RN [6]
RP STRUCTURE BY NMR OF 9-191.
RX MEDLINE-20283154; PubMed-10822252;
RA Hwang P.M., Vogel H.J.;
RT "Structures of the platelet calcium- and integrin-binding protein and
RT the alpha1b-integrin cytoplasmic domain suggest a mechanism for
RT calcium-regulated recognition; homology modelling and NMR studies.";
RL J. Mol. Recognit. 13:83-92(2000).
CC -1- FUNCTION: MAY CONVERT THE INACTIVE CONFORMATION OF INTEGRIN ALPHA-

```
CC IIB/BETA3 TO AN ACTIVE FORM THROUGH THE BINDING TO THE INTEGRIN
CC CYTOPLASMIC DOMAIN.
CC -1- SUBUNIT: INTERACTS WITH THE HETERODIMERIC INTEGRIN ALPHA-
CC IIB/BETA3. INTERACTS WITH THE PROTEIN KINASES SNK AND WITH THE
CC REGION IMMEDIATELY UPSTREAM OF THE KINASE DOMAIN OF DNA-PK.
CC -1- TISSUE SPECIFICITY: UBIQUITOUS.
CC -1- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U83236; AAB39758.1; -
DR EMBL; U85611; AAB53387.1; -
DR EMBL; U82226; AAC51106.1; -
DR EMBL; AB021866; BAA36281.1; -
DR EMBL; BC000846; AAH00846.1; -
DR PDB; 1DGV; 08-DEC-99.
DR Genew; HGNC:16920; CIB1.
DR MIM; 602293; -
DR InterPro; IPR002048; EF-hand.
DR Pfam; PF00036; ehand; 2.
DR ProDom; PD000012; EF-hand; 1.
DR SMART; SMO0054; EFh; 2.
DR PROSITE; PS00018; EF_HAND; 2.
KW Calcium-binding; Repeat; 3D-structure.
FT CA_BIND 116 127 EF-HAND 1 (POTENTIAL).
FT CA_BIND 161 172 EF-HAND 2 (POTENTIAL).
FT CONFLICT 44 44 T -> S (IN REF. 3 AND 5).
SQ SEQUENCE 191 AA; 21717 MW; 9AA6EA7897881E55 CRC64;

Query Match 99.8%; Score 955; DB 1; Length 191;
Best Local Similarity 99.5%; Pred. No. 2.2e-71;
Matches 190; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGGSGSRLSKELLAEQDLPFLTKQEILLAHRRFCELLPQEQRTVESLRAQVPEQILS 60
Db 1 MGGSGSRLSKELLAEQDLPFLTKQEILLAHRRFCELLPQEQRTVESLRAQVPEQILS 60
QY 61 LPELKPANPFKERICRVFSTSPAKDSLSFEDFLDLSVFSDTATPDIKSHYAFRIFDFFFDD 120
Db 61 LPELKPANPFKERICRVFSTSPAKDSLSFEDFLDLSVFSDTATPDIKSHYAFRIFDFFFDD 120
QY 121 GTLNREXLSRLVNCLTGEGEDTRLSASEMKQLIDNILEESDIDRDGTINLSEFQHVISR 180
Db 121 GTLNREXLSRLVNCLTGEGEDTRLSASEMKQLIDNILEESDIDRDGTINLSEFQHVISR 180
QY 181 PDFASSFKIVL 191
Db 181 PDFASSFKIVL 191

RESULT 2
KIPI_MOUSE
ID KIPI_MOUSE STANDARD; PRT; 191 AA.
AC Q920F4;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Calcium and integrin-binding protein 1 (Calmyrin) (DNA-PKcs
DE interacting protein) (Kinase interacting protein) (KIP) (CIB).
GN CIB1 OR PRKDCIP OR KIP OR CIB.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Kidney;
```

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RX MEDLINE-99069785; PubMed-9852683;
RA Seki N., Hayashi A., Abe M., Araki R., Fujimori A., Fukumura R.,
RA Hattori A., Kozuma S., Ohira M., Hori T., Saito T.;
RT "Chromosomal assignment of the gene for human DNA-PKcs interacting
RT protein (KIP) on chromosome 15q25.3-q26.1 by somatic hybrid analysis
RT and fluorescence in situ hybridization.";
RL J. Hum. Genet. 43:275-277(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Fetal kidney;
RX MEDLINE-99160477; PubMed-10051332;
RA Saito T., Seki N., Hattori A., Hayashi A., Abe M., Araki R.,
RA Fujimori A., Fukumura R., Kozuma S., Matsuda Y.;
RT "Structure, expression profile, and chromosomal location of a mouse
RT gene homologous to human DNA-PKcs interacting protein (KIP) gene.";
RL Mamm. Genome 10:315-317(1999).
RN [3]
RP SEQUENCE FROM N.A.
RA Naik M.U., Naik U.P.;
RT "Cloning and tissue distribution of murine calcium and integrin
RT binding protein, CIB.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RX MEDLINE-21085660; PubMed-11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaudo I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
CC -1- FUNCTION: MAY CONVERT THE INACTIVE CONFORMATION OF INTEGRIN ALPHA-
CC IIB/BETA3 TO AN ACTIVE FORM THROUGH THE BINDING TO THE INTEGRIN
CC CYTOPLASMIC DOMAIN (BY SIMILARITY).
CC -1- SUBUNIT: INTERACTS WITH THE HETERODIMERIC INTEGRIN ALPHA-
CC IIB/BETA3. INTERACTS WITH THE PROTEIN KINASES SNK AND WITH THE
CC REGION IMMEDIATELY UPSTREAM OF THE KINASE DOMAIN OF DNA-PK (BY
CC SIMILARITY).
CC -1- TISSUE SPECIFICITY: UBIQUITOUS.
CC -1- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AB006463; BAA74429.1; -
DR EMBL; AB017361; BAA36165.1; -
DR EMBL; AF173010; AAG38960.1; -
DR EMBL; AK010345; BAB26868.1; -
DR HSSP; Q99828; IDGV.
DR MGD; MGI:1344418; Cibl.
DR InterPro; IPR002048; EF-hand.
DR Pfam; PF00036; ehand; 2.
DR ProDom; PD000012; EF-hand; 1.
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DR SMART; SM00054; EFh; 2.
 DR PROSITE; PS00018; EF_HAND; 2.
 KW Calcium-binding; Repeat.
 FT CA_BIND 116 127 EF-HAND 1 (POTENTIAL).
 FT CA_BIND 161 172 EF-HAND 2 (POTENTIAL).
 SQ SEQUENCE 191 AA; 21763 MW; C85B603A19F9D9AC CRC64;

Query Match 94.3%; Score 902; DB 1; Length 191;
 Best Local Similarity 93.7%; Pred. No. 4.8e-67;
 Matches 179; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 MGGSGSRLSKELLAAYODLFTLKQEILLAHRRFCCELLPQEQRTVESSLRAQVPFEQILS 60
 Db 1 MGGSGSRLSKELLAAYODLFTLKQEILLAHRRFCCELLPQEQRTVESSLRAQVPFEQILS 60
 QY 61 LPELKANPKEKICRVFSTSPAKDSISFEDELDDLVSFSDTATPDIKSHYAFRIEFDDDD 120
 Db 61 LPELKANPKEKICRVFSTSPAKDSISFEDELDDLVSFSDTATPDIKSHYAFRIEFDDDD 120
 QY 121 GTLNREXLSRLVNCLTGEGEDTRLASASEMKOLIDNILEESDIDRDGTINLSEFQHVISRS 180
 Db 121 GTLDREDSLQLVNCLTGEEDTRLASASEMKOLIDNILEESDIDRDGTINLSEFQHVISRS 180
 QY 181 PDFASSFKIVL 191
 Db 181 PDFASSFKIVL 191

RESULT 3

KIP1_RAT
 ID KIP1_RAT STANDARD; PRT; 191 AA.

AC Q9R010; 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Calcium and Integrin-binding protein 1 (Calmyrin) (DNA-PKcs
 DE interacting protein) (kinase interacting protein) (KIP) (CIB).
 GN CIB1 OR PRKDCIP OR KIP OR CIB.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus;
 OX NCBI_TaxID=10116;

RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-99452760; PubMed-10523297;

RA Kauselmann G., Weiler M., Wulff P., Jessberger S., Konietzko U.,
 RA Scafield J., Staudil U., Bereliter-Hahn J., Strehardt K., Kuhl D.,
 RT "The polo-like protein kinases Fnk and Snk associate with a Ca(2+)-and
 RT integrin-binding protein and are regulated dynamically with synaptic
 RT plasticity.";
 RL EMBO J. 18:5528-5539(1999).

CC -1- FUNCTION: MAY CONVERT THE INACTIVE CONFORMATION OF INTEGRIN ALPHA-
 CC IIB/BETA3 TO AN ACTIVE FORM THROUGH THE BINDING TO THE INTEGRIN
 CC CYTOPLASMIC DOMAIN (BY SIMILARITY).
 CC -1- SUBUNIT: INTERACTS WITH THE HETERODIMERIC INTEGRIN ALPHA-
 CC IIB/BETA3. INTERACTS WITH THE PROTEIN KINASES SNK AND WITH THE
 CC REGION IMMEDIATELY UPSTREAM OF THE KINASE DOMAIN OF DNA-PK (BY
 CC SIMILARITY).
 CC -1- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.

CC -----
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DR EMBL; AF136585; AAF08368.1; -
 DR HSSP; Q99828; 1DGV.
 DR InterPro; IPR002048; EF-hand.
 DR Pfam; PF00036; ehand; 2.
 DR ProDom; PD000012; EF-hand; 1.

DR SMART; SM00054; EFh; 2.
 DR PROSITE; PS00018; EF_HAND; 2.
 KW Calcium-binding; Repeat.
 FT CA_BIND 116 127 EF-HAND 1 (POTENTIAL).
 FT CA_BIND 161 172 EF-HAND 2 (POTENTIAL).
 SQ SEQUENCE 191 AA; 21800 MW; 3B00B0228879FCC7 CRC64;

Query Match 94.1%; Score 901; DB 1; Length 191;
 Best Local Similarity 93.7%; Pred. No. 5.8e-67;
 Matches 179; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 1 MGGSGSRLSKELLAAYODLFTLKQEILLAHRRFCCELLPQEQRTVESSLRAQVPFEQILS 60
 Db 1 MGGSGSRLSKELLAAYODLFTLKQEILLAHRRFCCELLPQEQRTVESSLRAQVPFEQILS 60
 QY 61 LPELKANPKEKICRVFSTSPAKDSISFEDELDDLVSFSDTATPDIKSHYAFRIEFDDDD 120
 Db 61 LPELKANPKEKICRVFSTSPAKDSISFEDELDDLVSFSDTATPDIKSHYAFRIEFDDDD 120
 QY 121 GTLNREXLSRLVNCLTGEGEDTRLASASEMKOLIDNILEESDIDRDGTINLSEFQHVISRS 180
 Db 121 GTLDREDSLQLVNCLTGEEDTRLASASEMKOLIDNILEESDIDRDGTINLSEFQHVISRS 180
 QY 181 PDFASSFKIVL 191
 Db 181 PDFASSFKIVL 191

RESULT 4

KIP2_MOUSE
 ID KIP2_MOUSE STANDARD; PRT; 187 AA.

AC Q9Z309; 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Kinase interacting protein 2 (KIP 2).
 GN KIP2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;

RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain, and Testis;
 RX MEDLINE-99132027; PubMed-9931475;

RA Seki N., Hattori A., Hayashi A., Kozuma S., Ohira M., Hori T.,
 RA Saito T.,
 RT "Structure, expression profile and chromosomal location of an isolog
 RT of DNA-PKcs interacting protein (KIP) gene.";
 RL Blochm. Biophys. Acta 1444:143-147(1999).

CC -1- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
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CC -----
 CC EMBL; AB016080; BAA36545.1; -
 DR HSSP; Q99828; 1DGV.
 DR MGD; MGI:1929293; KIP2.
 DR InterPro; IPR002048; EF-hand.
 DR Pfam; PF00036; ehand; 3.
 DR ProDom; PD000012; EF-hand; 1.
 DR SMART; SM00054; EFh; 2.
 DR PROSITE; PS00018; EF_HAND; 2.
 DR Calcium-binding; Repeat.
 KW Calcium-binding; Repeat.
 FT CA_BIND 116 127 EF-HAND 1 (POTENTIAL).
 FT CA_BIND 157 168 EF-HAND 2 (POTENTIAL).
 SQ SEQUENCE 187 AA; 21703 MW; D21D21DCBD0B6F5C CRC64;


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Db      1 GAAPSKIVDGLLED-----TNFDRDEIERLRKRFRMKLRDRSSGSIDKN-----EFMSI 48
QY      62 PELKANPFKERICRVFSTSPAKDSLSEFEDFLDLLSVFSDTATPDIKSHYAFRIEDFDDG 1211
Db      49 PGVSSNPLAGRIMEYFADADNSGD-VDFQEFITGLSFSGRSGSKDEKLRFAPKIYDIDKDG 1077
QY      122 TLNREXLSRLVNCLTGEGEDTRLASASEMKOLIDNILEESDIDRDGTINLSEFQHY 177
Db      108 FISNGELFYIAKIMVG----SNLDEQLQIYDRTIVENDSDGDGRLSFEFEKNAI 159

RESULT 10
CALB_HUMAN
ID      CALB_HUMAN      STANDARD;      PRT;      169 AA.
AC      P06705; P15117; Q08044;
DT      01-JAN-1988 (Rel. 06, Created)
DT      01-APR-1990 (Rel. 14, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      Calcineurin B subunit isoform 1 (Protein phosphatase 2B regulatory
DE      subunit 1). (Protein phosphatase 3 regulatory subunit B alpha isoform
DE      1).
GN      PPP3R1 OR CNB OR CNA2.
OS      Homo sapiens (Human),
OS      Bos taurus (Bovine), and
OS      Rattus norvegicus (Rat).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxId=9606, 9913, 10116;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      SPECIES=Human;
RX      MEDLINE=90126237; PubMed=2558868;
RT      Guerini D., Krinks M.H., Sikela J.M., Hahn W.E., Klee C.B.;
RT      "Isolation and sequence of a cDNA clone for human calcineurin B, the
RT      Ca2+-binding subunit of the Ca2+/calmodulin-stimulated protein
RT      phosphatase.";
RL      DNA 8:675-682(1989).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      SPECIES=Human;
RX      Nargang C.E., Bottorff D.A., Adachi K.;
RL      Submitted (APR-1993) to the EMBL/GenBank/DBJ databases.
RN      [3]
RP      SEQUENCE OF 1-168.
RC      SPECIES=Bovine; TISSUE=Brain;
RX      MEDLINE=84132092; PubMed=6321184;
RT      Aitken A., Klee C.B., Cohen P.;
RT      "The structure of the B subunit of calcineurin.";
RL      Eur. J. Biochem. 139:663-671(1984).
RN      [4]
RP      SEQUENCE FROM N.A.
RC      SPECIES=Rat;
RX      Perrino B.A., Huang X., Ng L.Y., Soderling T.R.;
RL      Submitted (XXX-1992) to the EMBL/GenBank/DBJ databases.
RN      [5]
RP      SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RC      SPECIES=Rat; TISSUE=Brain, and Testis;
RX      MEDLINE=94153993; PubMed=8110831;
RT      Chang C.-D., Mukai H., Kuno T., Tanaka C.;
RT      "cDNA cloning of an alternatively spliced isoform of the regulatory
RT      subunit of Ca2+/calmodulin-dependent protein phosphatase (calcineurin
RT      B alpha 2).";
RL      Biochim. Biophys. Acta 1217:174-180(1994).
RN      [6]
RP      CALCIUM-BINDING DATA.
RC      SPECIES=Bovine;
RX      MEDLINE=80101597; PubMed=293720;
RT      Klee C.B., Crouch T.H., Krinks M.H.;
RT      "Calcineurin: a calcium- and calmodulin-binding protein of the
RT      nervous system.";
RL      Proc. Natl. Acad. Sci. U.S.A. 76:6270-6273(1979).
RN      [7]
RP      X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).

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Query Match	Best Local Similarity	Score	DB 1	Length
19.2%;	31.1%;	183.5;	DB 1;	169;
Pred.				


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DR EMBL; AK005067; BAB23791.1;...
DR HSSP; P06705; 1AUI.
DR MGD; MGI:1927185; Chp.
DR InterPro; IPR002048; EF-hand.
DR Pfam; PF00036; ehand; 3.
DR ProDom; PD000012; EF-hand; 2.
DR SMART; SM00054; EFh; 2.
DR PROSITE; PS00018; EF_HAND; 1.
KW Calcium-binding; Repeat; Myristate.
FT INIT_MET 0 0
FT LIPID 1 1 MYRISTATE (PROBABLE).
FT DOMAIN 38 49 ANCESTRAL CALCIUM SITE 1 (POTENTIAL).
FT DOMAIN 70 81 ANCESTRAL CALCIUM SITE 2 (POTENTIAL).
FT CA_BIND 122 133 EF-HAND 3 (BY SIMILARITY).
FT CA_BIND 163 174 EF-HAND 4 (BY SIMILARITY).
FT MUTAGEN 133 133 *E->A: LOSS OF TARGETING/FUSION FUNCTION.
SQ SEQUENCE 194 AA; 22301 MW; E2DF3E5F627B8231 CRC64;

Query Match 18.3%; Score 175; DB 1; Length 194;
Best Local Similarity 26.8%; Pred. No. 1.2e-07;
Matches 52; Conservative 34; Mismatches 76; Indels 32; Gaps 6;

QY 5 GSR----LSKELLAEQDITFLTQKEILLAHRRFCCELLPQEQTVESSLRAQVPFEQILS 60
Db 1 GSRASTLLRDEELEEKETGFSHQITRLYSRTSLDKGENTLSR-----EDFQR 52

QY 61 LPULKANPFKERICRVFSTSPAKDSLSFDFDILLSVF-----SDATPD----- 105
Db 53 IPELAINPLGDRINAF-FSEGEDQVFRGFMRTLAHFRPIEDNEKSKDVNGPEPLNSRS 111

QY 106 IKSHYAFRIFFDDGTLNREXLSRLVNLCTGEGEDTRLASSEMQLIDNILEESDIDRD 165
Db 112 NKLHFAFRLYDLKDKKISRDELLQVLRMVG---VNIQSDEQLGSIADRTIQEADQDGD 167

QY 166 GTINLSEFQHVISR 179
Db 168 SAISFTEFVKVLEK 181

RESULT 14
CALB_DROME STANDARD; PRT; 170 AA.
AC P48451; Q9W4D0;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Calcineurin B subunit, isoform 1 (Protein phosphatase 2B regulatory subunit)...
GN CANB OR CANB1 OR CNB1 OR CNB OR CG4209.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93054551; PubMed=1331060;
RA Guerini D., Montell C., Klee C.B.;
RT "Molecular cloning and characterization of the genes encoding the two subunits of Drosophila melanogaster calcineurin.";
RL J. Biol. Chem. 267:22542-22549(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
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Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W., Fosler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K., Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C., Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D., Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
CC -!- FUNCTION: CALCINEURIN IS A CALCIUM BINDING AND CALMODULIN BINDING PROTEIN FOUND IN ALL CELLS FROM YEAST TO MAMMALS, IT IS A CALCIUM DEPENDENT, CALMODULIN STIMULATED PROTEIN PHOSPHATASE (BY SIMILARITY).
CC -!- SUBUNIT: COMPOSED OF TWO COMPONENTS (A AND B), THE A COMPONENT IS THE CATALYTIC SUBUNIT AND THE B COMPONENT CONFERS CALCIUM SENSITIVITY (BY SIMILARITY).
CC -!- MISCELLANEOUS: THIS PROTEIN HAS FOUR FUNCTIONAL CALCIUM-BINDING SITES.
CC -!- SIMILARITY: TO OTHER EF-HAND CALCIUM BINDING PROTEINS.
CC -----
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CC -----
DR EMBL; M97215; AAA28411.1; -.
DR EMBL; AE003434; AAF46026.1; -.
DR HSSP; P06705; 1TCO.
DR FlyBase; FBgn0010014; CanB.
DR InterPro; IPR002048; EF-hand.
DR Pfam; PF00036; ehand; 4.
DR ProDom; PD000012; EF-hand; 2.
DR SMART; SM00054; EFh; 4.
DR PROSITE; PS00018; EF_HAND; 4.
KW Calcium-binding; Repeat.
FT CA_BIND 31 42 EF-HAND 1 (POTENTIAL).
FT CA_BIND 63 74 EF-HAND 2 (POTENTIAL).
FT CA_BIND 100 111 EF-HAND 3 (POTENTIAL).
FT CA_BIND 141 152 EF-HAND 4 (POTENTIAL).
SQ SEQUENCE 170 AA; 19341 MW; 77D89BE9BD961900 CRC64;

Query Match 17.9%; Score 171.5; DB 1; Length 170;
Best Local Similarity 26.5%; Pred. No. 2e-07;
Matches 41; Conservative 37; Mismatches 64; Indels 13; Gaps 3;

QY 26 EILLAHRRFCCELLPQEQTVESSLRAQVPFEQILSLPELKANPFKERICRVFSTSPAKDS 85
Db 19 EIRRLGKRF-----RKILDNSGALSIDFMSLPLOQNPLVQRVIDFD-ADGNGE 69
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QY 86 LSFEDFLDLVSFSDTATPDIKSHYAFRIFFDDDDGTNLNREXLSRLVNCLTGEGEDTRL 145
Db 70 VDFKEFIGVSQSFVRGDKLSKLRFAFRIDYNDNDGYISNGELFQVLKMYG-----NNLK 125
QY 146 ASEMQLIDNILESDIDRDGTINLSEFQHYISRS 180
Db 126 DTQLQIVDKTICFADKDEDGKISFDEFCVVGNT 160

RESULT 15
CA22_HUMAN
ID CA22_HUMAN STANDARD; PRT; 194 AA.
AC Q99653;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Calcium-binding protein p22 (Calcium-binding protein CHP) (Calcineurin
DE homologous protein) (Calcineurin B homolog).
GN CHP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=B-cell;
RX MEDLINE=97057295; PubMed=8901634;
RA Lin X., Barber D.L.;
RT "A calcineurin homologous protein inhibits GTPase-stimulated Na-H
RT exchange.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:12631-12636(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Muscle;
RA Strausberg R.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: REQUIRED FOR CONSTITUTIVE MEMBRANE TRAFFIC (BY
CC SIMILARITY). INHIBITS GTPASE-STIMULATED NA-H EXCHANGE.
CC SPECIFICALLY BINDS TO THE SODIUM/HYDROGEN EXCHANGER 1 (NHE1) AT A
CC DOMAIN THAT IS CRITICAL FOR GROWTH FACTOR STIMULATION OF EXCHANGE
CC ACTIVITY.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- TISSUE SPECIFICITY: UBQUITOUSLY EXPRESSED. HAS BEEN FOUND IN
CC FETAL EYE, LUNG, LIVER, MUSCLE, HEART, KIDNEY, THYMUS AND SPLEEN.
CC -!- PTM: BOTH N-MYRISTOYLATION AND CALCIUM-MEDIATED CONFORMATIONAL
CC CHANGES ARE ESSENTIAL FOR ITS FUNCTION IN EXOCYTIC TRAFFIC
CC (BY SIMILARITY).
CC -!- PTM: PHOSPHORYLATED IN VIVO. DECREASE IN ITS PHOSPHORYLATION IS
CC ASSOCIATED WITH AN INCREASE IN EXCHANGE ACTIVITY. THE
CC PHOSPHORYLATION STATE MAY REGULATE THE BINDING TO NHE1.
CC -!- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U61538; AAB37770.1; -
DR EMBL; BC001646; AAH01646.1; -
DR HSSP; P06705; LAUI.
DR MIM; 606988; -
DR InterPro; IPR002048; EF-hand.
DR Pfam; PF00036; efhand; 3.
DR ProDom; PD000012; EF-hand; 2.
DR SMART; SM00054; EFh; 2.
DR PROSITE; PS00018; EF_HAND; FALSE_NEG.
KW Calcium-binding; Repeat; Myristate; Phosphorylation.
FT INIT_MET 0
FT LIPID 1
FT DOMAIN 38 49 MYRISTATE (BY SIMILARITY).
FT ANCESTRAL CALCIUM SITE 1 (POTENTIAL).
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FT DOMAIN 70 81 ANCESTRAL CALCIUM SITE 2 (POTENTIAL).
FT CA_BIND 122 133 EF-HAND 3 (BY SIMILARITY).
FT CA_BIND 163 174 EF-HAND 4 (BY SIMILARITY).
SQ SEQUENCE 194 AA; 22325 MW; 17DDE5F03C88380 CRC64;

Query Match 17.8%; Score 170; DB 1; Length 194;
Best Local Similarity 26.3%; Pred. No. 3.2e-07;
Matches 51; Conservative 34; Mismatches 77; Indels 32; Gaps 6;

QY 5 GSR---LSKELLAEXQDLFTLTQKEILLAHRRCELLPQEQRTVESSLRACVPFEQILS 60
Db 1 GSRASTLLRDEELEIEIKKETGFSHSQITRLYSRFTSLDKGNGTISR-----EDFQR 52
QY 61 LPELKANPFKERICRVFSTSPAKDSLSEDFLDLSVF-----SDTATPD----- 105
Db 53 IPELAINPLGDRINAFPE-GEQVNFRRMRTLAHFRPIEDNEKSKDYNGPEPLNSRS 111
QY 106 IKSHYAFRIFFDDDDGTNLNREXLSRLVNCLTGEGEDTRLASASEMQLIDNILESDIDRD 165
Db 112 NKLHFAFRLYDDLDKDEKISRDELLQVLRMYG-----VNISDEQLGIADFTIQEADQGD 167
QY 166 GTINLSEFQHYISR 179
Db 168 SAISFTEFVKYLEK 181
```

Search completed: January 17, 2003, 12:42:25
Job time : 14 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 17, 2003, 12:42:04 ; Search time 17 Seconds
(without alignments)
1080.099 Million cell updates/sec

Title: MUT127
Perfect score: 957
Sequence: 1 MCGSGSRLSKELLAEXQDLT.....EFQHVISRSPDFASSFKIVL 191

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	406	42.4	311	2 T21563	hypothetical prote
2	207.5	21.7	174	2 T41632	probable calcineur
3	201.5	21.1	175	2 JH0462	phosphoprotein pho
4	196.5	20.5	174	2 T47245	calcineurin regula
5	183.5	19.2	170	1 A33391	calcineurin regula
6	183.5	19.2	170	1 S34127	calcineurin regula
7	183.5	19.2	170	1 JC1220	calcineurin regula
8	183.5	19.2	216	1 S42716	calcineurin regula
9	180.5	18.9	369	1 T22708	hypothetical prote
10	175.5	18.3	170	2 JC5174	calcineurin regula
11	172.5	18.0	170	2 JC7242	calcineurin regula
12	171.5	17.9	170	2 A44307	calcineurin regula
13	169.5	17.7	179	2 JC1221	calcineurin regula
14	167.5	17.5	165	2 PS0261	calcineurin regula
15	167.5	17.5	176	2 JQ1232	calcineurin regula
16	167.5	17.5	195	2 T28047	hypothetical prote
17	167.5	17.5	213	2 T31775	hypothetical prote
18	163.5	17.1	190	2 T20725	hypothetical prote
19	161.5	16.9	226	2 T51357	calcineurin B-like
20	153	16.0	190	2 T51686	calcineurin B-like
21	149.5	15.6	226	2 T08923	calcineurin B-like
22	148.5	15.5	213	2 T51356	calcineurin B-like
23	148	15.5	193	2 JH0816	neural vistin-11k
24	148	15.5	193	2 T50676	gene Rem-1 protein
25	148	15.5	246	2 T05308	hypothetical prote
26	148	15.5	246	2 H85387	hypothetical prote
27	147	15.4	193	2 S47565	calcium-binding pr
28	145	15.2	192	2 T01375	calcium sensor hom
29	142	14.8	190	2 A55666	neurocalcicn - frut

30	139	14.5	191	2 JH0815	neural vistin-11k
31	135.5	14.2	254	2 T29566	hypothetical prote
32	135	14.1	193	2 JC2186	hippocalcin - huma
33	135	14.1	270	2 JC7631	K+ channel-interac
34	134	14.0	224	2 F96668	protein FIN19.5 [1
35	132	13.8	193	2 JH0616	neurocalcicn (clone
36	132	13.8	195	2 JC1347	hippocalcin - rat
37	131	13.7	190	2 S58303	related to neurona
38	130	13.6	191	2 JH0605	neural vistin-11k
39	130	13.6	191	2 A48979	vistin-11k prote
40	128.5	13.4	172	2 S38531	caltracn - mouse
41	127	13.3	791	2 A53691	diacylglycerol kin
42	126	13.2	190	2 S61168	hypothetical prote
43	125.5	13.1	172	2 T38424	centrin - human
44	124	13.0	214	2 T08922	hypothetical prote
45	123.5	12.9	202	2 S21155	recoverin - mouse

ALIGNMENTS

RESULT 1
T21563
hypothetical protein F30A10.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T21563
R:Barlow, K.
submitted to the EMBL Data Library, October 1996
A:Reference number: Z19442
A:Accession: T21563
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-311 <WILL>
A:Cross-references: EMBL:Z81072; PIDN:CAB03019.1; GSPDB:GN00019; CESP:F30A10.1
A:Experimental source: clone F30A10
C:Genetics:
A:Gene: CESP:F30A10.1
A:Map position: 1
A:Introns: 106/2; 139/3; 190/3; 240/1

Query Match 42.4%; Score 406; DB 2; Length 311;
Best Local Similarity 42.0%; Pred. No. 8.3e-25;
Matches 87; Conservative 41; Mismatches 53; Indels 26; Gaps 5;

QY 1 MCGSGSRLS-----KELLAEXQDLFTLKQELLAHRRFCCELLPQEQRTVESS 48
DB 111 MGNNASSLSELNLFSGGVFTREQDDEYQDCFTFRKDIIRLYKRFYALNPK---VPTN 167
QY 49 LRAQVP-----FEQILSLPELKNPFKERICRVFSTSPAKDSLSEFEDLDLSVFSDTA 102
DB 168 MGNRPAITTLTFEEVEKMPLEKNPFKRRICEVFS-EDGRGNLSFDDFLDMFSVFSEMA 226
QY 103 TPDIKSHYAFRIFFDDDDGTINREXLSRLVNCITGEGEDTRLASASEMKQIDNILESDI 162
DB 227 PLQLKLYAFRIYIDGDELIGHDDLKMKIRSLTRD---ELSDVEVEFRIIEEADL 282
QY 163 DRDGTINLSEFQHVISRSPDFASSFKI 189
DB 283 DGDSSINFAEFHVSRSPPDFIRTFHI 309

RESULT 2
T41632
probable calcineurin b subunit - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 04-Feb-2000
C:Accession: T41632
R:McDougal, R.M.; Rajandream, M.A.; Barrell, B.G.; Rameperger, U.; Pohl, T.
submitted to the EMBL Data Library, August 1999
A:Reference number: Z22005
A:Accession: T41632
A>Status: preliminary; translated from GB/EMBL/DBJ

Best Local Similarity 26.1%; Pred. No. 1.4e-08;
Matches 41; Conservative 41; Mismatches 62; Indels 13; Gaps 3;
OY 24 KOEILLAHREPCCELLPOEQRTVESSLRAQVPEEQILSPELKANPFKERICRVSTSPAK 83
DB 20 REEVDRLEKRRHMKLDKNSGTIER-----EELSLPOISTNPLATRMIAIFDENGCG 71
OY 84 DLSLSEDFPDLILSVSDTATPDIKSHYAFRIFEDDDGTLNREXLSRLVNCLTGEGEDTR 143
DB 72 D-VDFQEFVSGLSAFSRKGNKEQKLRFAFKYDIDRDGYISNGELFVLMKMGV----SN 126
OY 144 LSASEMKOLIDNILEESDIDRDGTINLSEFQHYISRS 180
DB 127 LKDDQLQRIYDKTIMEADLDKDGKISFEFEFTKMENT 163
RESULT 5
A33391
Calcineurin regulatory chain - human
N:Alternate names: calcineurin beta subunit; calcineurin chain B; phosphoprotein phosphatase
C:Species: Homo sapiens (man)
C:Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 16-Jul-1999
C:Accession: A33391
R:Guerini, D.; Krinks, M.H.; Sikeia, J.M.; Hahn, W.E.; Klee, C.B.
DNA 8, 675-682, 1989
A:Title: Isolation and sequence of a cDNA clone for human calcineurin B, the Ca(2+)-binding protein
A:Reference number: A33391; MUID:90126237; PMID:2558868
A:Accession: A33391
A:Molecule type: mRNA
A:Residues: 1-170 <GUE>
A:Cross-references: GB:M30773; NID:g180704; PIDN:AAB08721.1; PID:g180705
C:Genetics:
A:Gene: GDB:PPP3R1; CALNB
A:Cross-references: GDB:136804; OMIM:601302
A:Map position: 2p16-2p15
C:Complex: heterodimer with calcineurin catalytic chain
C:Superfamily: calmodulin repeat homology
C:Keywords: blocked amino end; calcium binding; duplication; EF hand; heterodimer; 11p09
F:2-170/Product: calcineurin regulatory chain #status predicted <MAT>
F:18-49/Domain: calmodulin repeat homology <EF1>
F:50-82/Domain: calmodulin repeat homology <EF2>
F:87-119/Domain: calmodulin repeat homology <EF3>
F:128-160/Domain: calmodulin repeat homology <EF4>
F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F:3/Modified site: aspartic acid (Asn) #status predicted
F:31,33,35,37,42/Binding site: calcium (Asp, Asp, Ser, Ser, Glu) #status predicted
F:63,65,67,69,74/Binding site: calcium (Asp, Asp, Asn, Glu, Glu) #status predicted
F:100,102,104,106,111/Binding site: calcium (Asp, Asp, Tyr, Glu) #status predicted
F:141,143,145,147,152/Binding site: calcium (Asp, Asp, Arg, Glu) #status predicted
Query Match 19.2%; Score 183.5; DB 1; Length 170;
Best Local Similarity 31.1%; Pred. No. 1.4e-07;
Matches 38; Conservative 31; Mismatches 48; Indels 5; Gaps 2;
OY 56 EQILSLPELKANPFKERICRVSTSPAKDSLSFEDFLDLISVSDTATPDIKSHYAFRI 115
DB 41 EEFMSLPQLQNPVLRVIDIFDID-GNGEVDKFEFIEGVQSFSVKDGKQKLRFAFRIT 99
OY 116 DFDDGTLNREXLSRLVNCLTGEGEDTRLASASEMKOLIDNILEESDIDRDGTINLSEFQH 175
DB 100 DMDKDGYSISNGELFQVLMKMGV----NNLKDTQLQIYDKTIINADKDGGRISFEFCA 155
OY 176 VI 177
DB 156 VV 157
RESULT 6
S34127
Calcineurin regulatory chain [validated] - bovine
N:Alternate names: calcineurin beta subunit; calcineurin chain B; phosphoprotein phosphatase
C:Species: Bos primigenius taurus (cattle)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 15-Sep-2000

C:Accession: I45831; JT0297; S34127
R:Nargang, C.E.; Bottorff, D.A.; Adachi, K.
DNA Seq. 4, 313-318, 1994
A:Title: Isolation and characterization of a cDNA clone coding for the calcium-binding protein
A:Reference number: I45831; MUID:95102111; PMID:7803816
A:Accession: I45831
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-170 <NA2>
A:Cross-references: EMBL:X71666; NID:g312968; PIDN:CAA50659.1; PID:g312969
R:Altken, A.; Klee, C.B.; Cohen, P.
Eur. J. Biochem. 139, 663-671, 1984
A:Title: The structure of the B subunit of calcineurin.
A:Reference number: JT0297; MUID:84132092; PMID:6321184
A:Accession: JT0297
A:Molecule type: protein
A:Residues: 2-11, 'M', 13-153, 'S', 155-169 <AIT>
R:Griffith, J.P.; Kim, J.L.; Kim, E.E.; Shtuchak, M.D.; Thomson, J.A.; Fitzgibbon, submitted to the Brookhaven Protein Data Bank, August 1996
A:Reference number: A66708; PDB:1TCO
A:Contents: annotation; X-ray crystallography, 2.5 angstroms
C:Superfamily: calmodulin; calmodulin repeat homology
C:Keywords: blocked amino end; calcium binding; duplication; EF hand; heterodimer; 11p09
F:2-170/Product: calcineurin regulatory chain #status experimental <MAT>
F:18-49/Domain: calmodulin repeat homology <EF1>
F:50-82/Domain: calmodulin repeat homology <EF2>
F:87-119/Domain: calmodulin repeat homology <EF3>
F:128-160/Domain: calmodulin repeat homology <EF4>
F:2/Modified site: myristylated amino end (Gly) (in mature form) #status experiment
F:3/Modified site: aspartic acid (Asn) #status predicted
F:31,33,35,37,42/Binding site: calcium (Asp, Asp, Ser, Ser, Glu) #status experiment
F:63,65,67,69,74/Binding site: calcium (Asp, Asp, Asn, Glu, Glu) #status experiment
F:100,102,104,106,111/Binding site: calcium (Asp, Asp, Tyr, Glu) #status experiment
F:141,143,145,147,152/Binding site: calcium (Asp, Asp, Arg, Glu) #status experiment
Query Match 19.2%; Score 183.5; DB 1; Length 170;
Best Local Similarity 31.1%; Pred. No. 1.4e-07;
Matches 38; Conservative 31; Mismatches 48; Indels 5; Gaps 2;
OY 56 EQILSLPELKANPFKERICRVSTSPAKDSLSFEDFLDLISVSDTATPDIKSHYAFRI 115
DB 41 EEFMSLPQLQNPVLRVIDIFDID-GNGEVDKFEFIEGVQSFSVKDGKQKLRFAFRIT 99
OY 116 DFDDGTLNREXLSRLVNCLTGEGEDTRLASASEMKOLIDNILEESDIDRDGTINLSEFQH 175
DB 100 DMDKDGYSISNGELFQVLMKMGV----NNLKDTQLQIYDKTIINADKDGGRISFEFCA 155
OY 176 VI 177
DB 156 VV 157
RESULT 7
JC1220
Calcineurin regulatory chain, brain - mouse
N:Alternate names: calcineurin beta-1 subunit; calcineurin chain B-1; phosphoprotein
C:Species: Mus musculus (house mouse)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: JC1220
R:Ueki, K.; Muramatsu, T.; Kincaid, R.L.
Biochem. Biophys. Res. Commun. 187, 537-543, 1992
A:Title: Structure and expression of two isoforms of the murine calmodulin-dependent protein kinase
A:Reference number: JC1220; MUID:92392379; PMID:1325794
A:Accession: JC1220
A:Molecule type: mRNA
A:Residues: 1-170 <UEK>
A:Cross-references: GB:S43864; NID:g255078; PIDN:AAB23171.1; PID:g255079

A;Experimental source: brain
C;Comment: With calcineurin catalytic chain plays an important role in neural and nonneu
C;Genetics:
A;Gene: PP2B-beta-1
C;Complex: heterodimer with calcineurin catalytic chain
C;Superfamily: calmodulin; calmodulin repeat homology
C;Keywords: blocked amino end; calcium binding; duplication; EF hand; heterodimer; lipop
F;2-170/Product: calcineurin regulatory chain #status predicted <MAT>
F;18-49/Domain: calmodulin repeat homology <EF1>
F;50-82/Domain: calmodulin repeat homology <EF2>
F;87-119/Domain: calmodulin repeat homology <EF3>
F;128-160/Domain: calmodulin repeat homology <EF4>
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted

Query Match 19.2%; Score 183.5; DB 1; Length 170;
Best Local Similarity 31.1%; Pred. No. 1.4e-07;
Matches 38; Conservative 31; Mismatches 48; Indels 5; Gaps 2;

QY 56 EQILSLPELKANPFKERICRVFSTSPAKDSLSFEDFLDLLSVFSDTATPDIKSHYAFRIF 115
Db 41 EEFMSLPELQONPLVQVRVIDFTD-GNGEVDFEFIEGVSVKSGDKKEQKLRFAFRIF 99

QY 116 DFDDGGTLNREXLSRLVNCLTGEGEDTRLSASEMKQLIDNILEESDIDRDGTINLSEFQH 175
Db 100 DMDKDGYSINGELFQVLKMMVG-----NNLKDQLQOIIVDKTIINADKDGGRISFEFCA 155

QY 176 VI 177
Db 156 VV 157

RESULT 8
S42716
calcineurin regulatory chain, long splice form - rat
N;Alternate names: calcineurin beta subunit; calcineurin chain B; phosphoprotein phosph
N;Contains: calcineurin regulatory chain, short splice form
C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C;Accession: S42716; S42717
R;Chang, C.D.; Mukai, H.; Kuno, T.; Tanaka, C.
Biochim. Biophys. Acta 1217, 174-180, 1994
A;Title: cDNA cloning of an alternatively spliced isoform of the regulatory subunit of C
A;Reference number: S42716; MUID:94153993; PMID:8110831
A;Accession: S42716
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-216 <CHAL>
A;Cross-references: EMBL:D14425; NID:g286205; PIDN:BAA03318.1; PID:g286206
A;Accession: S42717
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 'M',48-216 <CHA2>
A;Cross-references: EMBL:D14568; NID:g286255; PIDN:BAA03422.1; PID:g286256
C;Complex: heterodimer with calcineurin catalytic chain
C;Superfamily: calmodulin; calmodulin repeat homology
C;Keywords: alternative splicing; blocked amino end; calcium binding; duplication; EF ha
F;2-216/Product: calcineurin regulatory chain, long splice form #status predicted <MATL>
F;48-216/Product: calcineurin regulatory chain, short splice form #status predicted <MAT
F;64-95/Domain: calmodulin repeat homology <EF1>
F;96-128/Domain: calmodulin repeat homology <EF2>
F;'M',48-216/Product: calcineurin regulatory chain, short splice form precursor #status
F;133-165/Domain: calmodulin repeat homology <EF3>
F;174-206/Domain: calmodulin repeat homology <EF4>
F;48/Modified site: myristylated amino end (Gly) (in mature form) #status experimental
F;49/Modified site: aspartic acid (Asn) #status predicted

Query Match 19.2%; Score 183.5; DB 1; Length 216;
Best Local Similarity 31.1%; Pred. No. 1.9e-07;
Matches 38; Conservative 31; Mismatches 48; Indels 5; Gaps 2;

QY 56 EQILSLPELKANPFKERICRVFSTSPAKDSLSFEDFLDLLSVFSDTATPDIKSHYAFRIF 115
Db 87 EEFMSLPELQONPLVQVRVIDFTD-GNGEVDFEFIEGVSVKSGDKKEQKLRFAFRIF 145

QY 116 DFDDGGTLNREXLSRLVNCLTGEGEDTRLSASEMKQLIDNILEESDIDRDGTINLSEFQH 175
Db 146 DMDKDGYSINGELFQVLKMMVG-----NNLKDQLQOIIVDKTIINADKDGGRISFEFCA 201

QY 176 VI 177
Db 202 VV 203

RESULT 9
T22708
hypothetical protein F55C10.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T22708
R;Dobson, R.
submitted to the EMBL Data Library, June 1996
A;Reference number: Z19603
A;Accession: T22708
A;Status: preliminary; translated from GB/EMBL/DBBJ
A;Molecule type: DNA
A;Residues: 1-369 <WIL>
A;Cross-references: EMBL:Z74036; PIDN:CAA98489.1; GSPDB:GN00023; CESP:F55C10.1
A;Experimental source: clone F55C10
C;Genetics:
A;Gene: CESP:F55C10.1
A;Map position: 5
A;Introns: 159/2; 199/3; 213/1; 272/1; 312/3; 353/3

Query Match 18.9%; Score 180.5; DB 2; Length 369;
Best Local Similarity 27.8%; Pred. No. 6.1e-07;
Matches 50; Conservative 37; Mismatches 70; Indels 23; Gaps 6;

QY 3 GSGSRLSKELLAEQ--DLTFLTKQEILLAHRRFCELLPQORTVSESSLRAQVPFEQILS 60
Db 200 GADASLPMECMCSNFDAYELRLT-----RRFKKL-----DVDGS--GSLSVVEEFMS 243

QY 61 LPELKANPFKERICRVFSTSPAKDSLSFEDFLDLLSVFSDTATPDIKSHYAFRIFDEDD 120
Db 244 LPELQONPLVQVRVIDIFD-EDNGEVDREFIQISQFSVKGDKNKTKLFAFRIDMDRD 302

QY 121 GTLNREXLSRLVNCLTGEGEDTRLSASEMKQLIDNILEESDIDRDGTINLSEFQHVISR 180
Db 303 GFISNGELFQVLKMMVG-----NNLKDSQLQOIIVDKTILFHDKDGDKISFQECFCDVVEHT 358

RESULT 10
JC5174
calcineurin regulatory chain 2 - fruit fly (Drosophila melanogaster)
N;Alternate names: calcineurin beta subunit; calcineurin chain B-2; phosphoprotein f
C;Species: Drosophila melanogaster
C;Date: 16-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 13-Aug-1999
C;Accession: JC5174
R;Warren, W.D.; Phillips, A.M.; Howells, A.J.
Gene 177, 149-153, 1996
A;Title: Drosophila melanogaster contains both X-linked and autosomal homologues of
A;Reference number: JC5174; MUID:97080515; PMID:8921860
A;Accession: JC5174
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-170 <WAR>
A;Cross-references: GB:U56245; NID:g1336009; PIDN:AAC47350.1; PID:g1336010
C;Comment: This protein is the calcium binding chain of calcineurin, involved in cal
C;Genetics:
A;Gene: dCnB2
C;Complex: heterodimer with calcineurin catalytic chain
C;Superfamily: calmodulin; calmodulin repeat homology
C;Keywords: blocked amino end; calcium binding; duplication; EF hand; heterodimer; l
F;2-170/Product: calcineurin regulatory chain #status predicted <MAT>
F;18-49/Domain: calmodulin repeat homology <EF1>
F;50-82/Domain: calmodulin repeat homology <EF2>
F;87-119/Domain: calmodulin repeat homology <EF3>

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OM protein - protein search, using sw model

Run on: January 17, 2003, 12:42:04 ; Search time 15 Seconds
(without alignments)
374.652 Million cell updates/sec

Title: MUT127
Perfect score: 957
Sequence: 1 MGGSGSRLSKELLAERYDLT.....EFQHVISRSPDFASSFKIVL 191

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA.*
1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep.*
2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	951	99.4	191	4	US-08-720-625-2 Sequence 2, Appl1
2	945	98.7	191	3	US-08-764-563-1 Sequence 1, Appl1
3	213.5	22.3	177	3	US-08-764-563-3 Sequence 3, Appl1
4	201.5	21.1	174	1	US-08-328-322-17 Sequence 17, Appl1
5	190.5	19.9	157	1	US-08-328-322-15 Sequence 15, Appl1
6	183.5	19.2	169	4	US-08-720-625-4 Sequence 5, Appl1
7	183.5	19.2	170	3	US-08-764-563-5 Sequence 8, Appl1
8	173	18.1	186	3	US-08-655-352-8 Sequence 8, Appl1
9	173	18.1	186	4	US-09-257-825B-8 Sequence 8, Appl1
10	173	18.1	186	4	US-09-257-825B-8 Sequence 8, Appl1
11	169.5	17.7	179	3	US-08-764-563-4 Sequence 4, Appl1
12	150.5	15.7	196	3	US-09-048-889-1 Sequence 1, Appl1
13	147	15.4	193	3	US-08-655-352-3 Sequence 3, Appl1
14	147	15.4	193	4	US-09-258-016-3 Sequence 3, Appl1
15	147	15.4	193	4	US-09-257-825B-3 Sequence 3, Appl1
16	140	14.6	220	4	US-09-399-913-26 Sequence 26, Appl1
17	140	14.6	220	4	US-09-298-731-26 Sequence 26, Appl1
18	139	14.5	191	3	US-08-655-352-7 Sequence 7, Appl1
19	139	14.5	191	4	US-09-258-016-7 Sequence 7, Appl1
20	139	14.5	191	4	US-09-257-825B-7 Sequence 7, Appl1
21	136	14.2	193	3	US-08-655-352-2 Sequence 2, Appl1
22	136	14.2	193	4	US-09-258-016-2 Sequence 2, Appl1
23	135	14.1	193	4	US-09-257-825B-2 Sequence 2, Appl1
24	135	14.1	216	4	US-09-399-913-6 Sequence 6, Appl1
25	135	14.1	216	4	US-09-298-731-6 Sequence 6, Appl1
26	135	14.1	220	4	US-09-399-913-24 Sequence 24, Appl1
27	135	14.1	220	4	US-09-298-731-24 Sequence 24, Appl1

28	135	14.1	227	4	US-09-399-913-8	Sequence 8, Appl1
29	135	14.1	227	4	US-09-399-913-10	Sequence 10, Appl1
30	135	14.1	227	4	US-09-298-731-8	Sequence 8, Appl1
31	135	14.1	227	4	US-09-298-731-10	Sequence 10, Appl1
32	135	14.1	245	4	US-09-399-913-4	Sequence 4, Appl1
33	135	14.1	245	4	US-09-298-731-4	Sequence 4, Appl1
34	135	14.1	252	4	US-09-399-913-20	Sequence 20, Appl1
35	135	14.1	252	4	US-09-298-731-20	Sequence 20, Appl1
36	135	14.1	270	4	US-09-399-913-14	Sequence 14, Appl1
37	135	14.1	270	4	US-09-298-731-14	Sequence 14, Appl1
38	134	14.0	216	4	US-09-399-913-2	Sequence 2, Appl1
39	134	14.0	216	4	US-09-298-731-2	Sequence 2, Appl1
40	132	13.8	270	4	US-09-399-913-18	Sequence 18, Appl1
41	132	13.8	270	4	US-09-298-731-18	Sequence 18, Appl1
42	131	13.7	193	3	US-08-655-352-4	Sequence 4, Appl1
43	131	13.7	193	4	US-09-258-016-4	Sequence 4, Appl1
44	131	13.7	193	4	US-09-257-825B-4	Sequence 4, Appl1
45	130	13.6	191	3	US-08-655-352-5	Sequence 5, Appl1

ALIGNMENTS

RESULT 1
US-08-720-625-2
Sequence 2, Application US/08720625
Patent No. 6242587

GENERAL INFORMATION:

APPLICANT: Naik, Ulhas P.
APPLICANT: Parise, Leslie V.
TITLE OF INVENTION: CALCIUM-INTEGRIN BINDING PROTEIN
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bell, Seltzer, Park & Gibson
STREET: P.O. Drawer 34009
CITY: Charlotte
STATE: No. 6242587th Carolina
COUNTRY: USA
ZIP: 28234

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/720,625
FILING DATE:
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5470-138
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-420-2200
TELEFAX: 919-881-3175

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
LENGTH: 191 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-720-625-2

Query Match 99.4%; Score 951; DB 4; Length 191;
Best Local Similarity 99.0%; Pred. No. 4, 8e-99;
Matches 189; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGGSGSRLSKELLAERYDLTFLTKQELLAHRRCELLPQEQRTVESSLRAQVPEQILS 60
Db 1 MGGSGSRLSKELLAERYDLTFLTKQELLAHRRCELLPQEQRSVSSLRAQVPEQILS 60
QY 61 LPELKNPFKERICRYFTSPAKDSLSEDFDLISVSDTATPDIKSHYAFRIEDFDDDD 120
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Db 61 LPELKANPFKERICRVFSTPAKDSLSFEDFLDLLSVFSDTATPDIKSHYAFRIFDFFF 120
QY 121 GTLNREXLSRLVNLCTGEGEDTRLSASEMKQLIDNILEESDIDRDGTINLSEFQHVISR 180
Db 121 GTLNREXLSRLVNLCTGEGEDTRLSASEMKQLIDNILEESDIDRDGTINLSEFQHVISR 180
QY 181 PDFASSFKIVL 191
Db 181 PDFASSFKIVL 191

RESULT 2

US-08-764-563-1
; Sequence 1, Application US/08764563
; Patent No. 6093565
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: A NOVEL PROTEIN PHOSPHATASE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; FILING DATE: Herewith
; APPLICATION NUMBER: US/08/764,563
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0178 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 191 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: Consensus
; CLONE: Consensus
US-08-764-563-1

Query Match 98.7%; Score 945; DB 3; Length 191;
Best Local Similarity 98.4%; Pred. No. 2.3e-98;
Matches 188; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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Db 1 MGGSGSRLSKELLAQYDLTFLTKQELLAHRRFCELLPQEQRTVLESSLRAQVPFEQILS 60
QY 61 LPELKANPFKERICRVFSTPAKDSLSFEDFLDLLSVFSDTATPDIKSHYAFRIFDFFF 120
Db 61 LPELKANPFKERICRVFSTPAKDSLSFEDFLDLLSVFSDTATPDIKSHYAFRIFDFFF 120
QY 121 GTLNREXLSRLVNLCTGEGEDTRLSASEMKQLIDNILEESDIDRDGTINLSEFQHVISR 180
Db 121 GTLNREXLSRLVNLCTGEGEDTRLSASEMKQLIDNILEESDIDRDGTINLSEFQHVISR 180

QY 181 PDFASSFKIVL 191
Db 181 PDFASSFKIVL 191
RESULT 3
US-08-764-563-3
; Sequence 3, Application US/08764563
; Patent No. 6093565
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: A NOVEL PROTEIN PHOSPHATASE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/764,563
; FILING DATE: Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0178 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 177 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 458230
US-08-764-563-3

Query Match 22.3%; Score 213.5; DB 3; Length 177;
Best Local Similarity 29.2%; Pred. No. 2.9e-16;
Matches 52; Conservative 39; Mismatches 74; Indels 13; Gaps 3;
QY 1 MGGSGSRLSKELLAQYDLTFLTKQELLAHRRFCELLPQEQRTVLESSLRAQVPFEQILS 60
Db 1 MGTNTSSLRPEEVEEMQGTNFTQKEIKKLYKRFKLKDNGNGTISK-----DEFLM 52
QY 61 LPELKANPFKERICRVFSTPAKDSLSFEDFLDLLSVFSDTATPDIKSHYAFRIFDFFF 120
Db 53 IPELAVNPLVKRVISIFDEN-GDGSVNFKEFIAALSVEFNAQGDQKQKLEFAFKVYDIDGD 111
QY 121 GTLNREXLSRLVNLCTGEGEDTRLSASEMKQLIDNILEESDIDRDGTINLSEFQHVISR 178
Db 112 GYISNGELFTVLKMMVG---NNLSDVQLQQIVDKTILEADEGDGDKISFEFAKTL 165
RESULT 4
US-08-328-322-17
; Sequence 17, Application US/08328322

```
Patent No. 5723436
GENERAL INFORMATION:
APPLICANT: Huang, Laiqiang
APPLICANT: Cyert, Martha S.
TITLE OF INVENTION: Calcineurin Interacting Protein Compositions
TITLE OF INVENTION: and Methods
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/328,322
FILING DATE: 24-OCT-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: P38,615
REFERENCE/DOCKET NUMBER: 8600-0151.10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-328-322-17

Query Match      21.1%; Score 201.5; DB 1; Length 174;
Best Local Similarity 27.1%; Pred. No. 6.3e-15;
Matches 48; Conservative 43; Mismatches 69; Indels 17; Gaps 4;

QY 1 MGGSGRSLKELLAQYQDLTFLKQELLAHRRFCCLLPQQRVYESSLRAQVPEQILS 60
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QY 61 LPELKANPKEKRICRVSTSPAKDSLSFEDFLDLVSFSDTATPDIKSHYAFRIEDFDD 120
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QY 121 GTLNREXLSRLVNCLTGEGETRLSASEMKOLIDNILESDIDRDGTINLSEFOHVI 177
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Db 108 GFISNGELFIVLKIMVG---SNLDDEQLQOIVRTIVENDSDGDGRLSFEFFKNAI 160

RESULT 5
US-08-328-322-15
Sequence 15, Application US/08328322
Patent No. 5723436
GENERAL INFORMATION:
APPLICANT: Huang, Laiqiang
APPLICANT: Cyert, Martha S.
TITLE OF INVENTION: Calcineurin Interacting Protein Compositions
TITLE OF INVENTION: and Methods
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/328,322
FILING DATE: 24-OCT-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: P38,615
REFERENCE/DOCKET NUMBER: 8600-0151.10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 157 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-328-322-15

Query Match      19.9%; Score 190.5; DB 1; Length 157;
Best Local Similarity 27.3%; Pred. No. 9.3e-14;
Matches 42; Conservative 39; Mismatches 60; Indels 13; Gaps 3;

QY 24 KOELLAHRRFCCLLPQQRVYESSLRAQVPEQILSLPELKANPKEKRICRVSTSPAK 83
  :|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 3 RDEIERLRKRFMKLDRDSSGSDKN-----EFMSIPGVSSNPLAGRIMEVFADADNSG 54

QY 84 DLSFEDFLDLVSFSDTATPDIKSHYAFRIEDFDDGTNLNREXLSRLVNCLTGEGETR 143
  |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 55 D-VDFQEFITGLSIFSGSGSKDEKLRFKFIYDIDKGFISNGELFIVLKIMVG---SN 109

QY 144 LSASEMKOLIDNILESDIDRDGTINLSEFOHVI 177
  |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 110 LDDEQLQOIVRTIVENDSDGDGRLSFEFFKNAI 143

RESULT 6
US-08-720-625-4
Sequence 4, Application US/08720625
Patent No. 6242587
GENERAL INFORMATION:
APPLICANT: Naik, Ulhas P.
APPLICANT: Parise, Leslie V.
TITLE OF INVENTION: CALCITUM-INTEGRIN BINDING PROTEIN
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bell, Seltzer, Park & Gibson
STREET: P.O. Drawer 34009
CITY: Charlotte
STATE: No. 6242587th Carolina
COUNTRY: USA
ZIP: 28234
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/720,625
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5470-138
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-420-2200
TELEFAX: 919-881-3175
INFORMATION FOR SEQ ID NO: 4:
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```

QY      61 LPELKANPFKERICRVFSTSPAKDLSFEDELDLLSVFSDTATPDIKSHYAFRIEDFDD 120
      1:  :  |  :  ||  :  ||  :  ||  :  ||  :  ||  :  ||  :  ||  :  ||
Db      56 PPOGDPSKFASLVRVEDEN-NDGSTIEFEERIALSVTSKGL--DEKLQMAFRLYDVND 112
QY      121 GTLNREXLSRLVNCL-----TGEGEDTRLASASEMKOLIDNILEESDIDRGTLNSE 172
      1:  :  ||  :  ||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db      113 GYITREMYNINIVDAIYQMGQGPQSEIDENT-----PQKRVDKIFDQMDKNHDKLTLEE 166
QY      173 FOHVISRSPDFASSFKI 189
      1:  :  |  :  :  :
Db      167 FREGSKADPRIVQALSL 183

```

RESULT 9
US-09-258-016-8
; Sequence 8, Application US/09258016
; Patent No. 6362395

GENERAL INFORMATION:
APPLICANT: Bachettiira W. Poovaiyah, Zhinhua Liu,
APPLICANT: Shameekumar Patil, Daisuke Takezawa
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: PRODUCTION OF MALE-STERILE PLANTS
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klarquist Sparkman Campbell Leigh &
ADDRESSEE: Winston, LLP
STREET: One World Trade Center
STREET: 121 S.W. Salmon Street
STREET: Suite 1600
CITY: Portland
STATE: Oregon
COUNTRY: United States of America
ZIP: 97204
COMPUTER READABLE FORM:
MEDIUM TYPE: Disk, 3-1/2 inch
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/258, 016

```

: FILING DATE:
: CLASSIFICATION:
: ATTORNEY/AGENT INFORMATION:
: NAME: Stephens Jr., Donald L.
: REGISTRATION NUMBER: 34,022
: REFERENCE/DOCKET NUMBER: 4630-51994
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (503) 226-7391
: TELEFAX: (503) 228-9446
: INFORMATION FOR SEQ ID NO: 8:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 186 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: DESCRIPTION: Region of Drosophila frequen
: DESCRIPTION: (Gen2:Drofreg) with homology to lily
: ;
: ;
US-09-258-016-8

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Query Match	18.1%;	Score 173;	DB 4;	length 186;
Best Local Similarity	25.4%;	Pred. No. 1.1e-11;		
Matches 50; Conservative	39;	Mismatches 86;	Indels 33.	Canc

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QY      1 MGGSGSRLSKELLAEYODLTFTLKOEILLAHRCCELLPQEQRTVESSLRAQVPFEQILS 60
      ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
Db      1 MGKSSSKLKQDIDRLTTDTYFTEKEIRQWHKGFLLKDCPNGLLTQGFIKIYKQF----- 55

QY      61 LPELKANDEKERICRVFSTSPAKDLSFEDEFLDLLSVFSDTATPDIKSHYAFRIFEDEDD 120
      ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
Db      56 FPQGDPSKFAFLVRFVDEN-NDGSIIEFEFIRALSVTSKGL--DEKLQWAFRLYDVND 1122
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QY      121 GTLNREKLSRLVNCI-----TGECDTRLASASEMKQLIDNILESDIDRDGTINSE 172
        | : || : ::| : | | :||
Db      113 GYTREMYNIYDAIYQWVGQQPQSEDNT-----PKRVDKIFDQMDKNHDKGLTLFE 166
        | : || : ::| : | | :||
QY      173 FQHVISRSPDFASSFKI 189
        | : || : ::| : | | :||
Db      167 FREGSKADPRIVQALSL 183
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RESULT 10
US-09-257-825B-8
Sequence 8, Application US/09257825B

```

; Patent NO.: 6403352
; GENERAL INFORMATION:
; APPLICANT: Poovalah, Bachettlira W.
; APPLICANT: Patil, Shameekumar
; APPLICANT: Takezawa, Daisuke
; TITLE OF INVENTION: Compositions and Methods for Production of Male-Sterile Plant
; FILE REFERENCE: 4630-51993
; CURRENT APPLICATION NUMBER: US/09/257,825B
; PRIOR FILING DATE: 1999-02-25
; PRIOR APPLICATION NUMBER: US 08/655,352
; PRIOR FILING DATE: 1996-05-23
; PRIOR APPLICATION NUMBER: US 60/014,743
; PRIOR FILING DATE: 1996-03-28
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 186
; TYPE: PRT
; ORGANISM: Drosophila
US-09-257-825B-8

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Query Match	18.1%;	Score 173;	DB 4;	Length 186;
Best Local Similarity	25.48%;	Pred. No. 1,1e-11;		
Matches 50;	Conservative 39;	Mismatches 86;	Indels 22;	Gaps 5.

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QY      1 MGGSGSRLSKELLAEYODTFLTKOETILLAHRRFCCELLPOEORTVESSLRAQPPEEQILS   60  
        || | : : : | : | : | | : : |  
Db      1 MGKKSSKLKODTIDRLTTDTYTETEKEIRQWHKGFCLKDCPNGILTTEGFIKIYKQF-----   55  
  
QY      61 LPBLKANDEKERICRVFSTSPAKDSISFEDELDLLSVFSDFATPDIKSHYAFRIFEDDDD   120  
        | : : | : ||| : | : | : | | | | :||| : | : |  
Db      56 FPQGDPSPKFASLVERVFEDEN-NDGSLEEFEEFIRALSVTSKGL--DEKLQWAFLRYDVAND.   112  
  
QY      121 GTLNREXSLRVLNCL-----TGEGEDTRLASASEMKQLDINILEESDIDRDGTINISE   172  
        | : || : | : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |  
Db      113 GYTIREEMYNIVDAIQWMVGQQPOSEDENT-----PQRVDKIFDQMDKNHDKLTLEE   166  
  
QY      173 FQHVISRSPDPFASSFKEI    189  
        | : | : | : :  
Db      167 FRFGSKADPRIVOALS     183
```

RESULT 11
US-08-764-563-4

Sequence 4, Application US/08764563
Patent No. 6033565
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Goll, Surya K.
TITLE OF INVENTION: A NOVEL PROTEIN PHOSPHATASE
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/323,449
 FILING DATE: October 14, 1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Dow, Alan. E.
 REGISTRATION NUMBER: 35,123
 REFERENCE/DOCKET NUMBER: 4630-45000
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (503) 226-7391
 TELEFAX: (503) 228-9446
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 193 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 DESCRIPTION: Region of rat neural vlslnln-like protein
 DESCRIPTION: (Gen2:Ratnvp3) with homology to lily
 DESCRIPTION: CCAMK
 US-08-655-352-3

Query Match 15.4%; Score 147; DB 3; Length 193;
 Best Local Similarity 24.5%; Pred. No. 9.7e-09;
 Matches 51; Conservative 41; Mismatches 80; Indels 36; Gaps 7;

QY 1 MGGSGRLSKELLAAYQDLFLTKQELLAHRRCELLPQEQRTVESSLRAQVFEQILS 60
 DB 1 MGKQNSKLRPEVLQDLREHTEFTDHELQEWYKGLKDCPTGHLTYDE-----FKKIYA 53
 QY 61 --LPELKANPEKERICRVSTSPAKDSLSFEFLLSVFSDTATPDIKSHYAFRIFFD 118
 DB 54 NFFPYGDAKFAEHVFTFDIN-SDGTIDFREFIALLSVTS-RGKLEQIKWAFSMYDLD 111
 QY 119 DDGTLNREXLSRLVNLGEGEDTRLASASEM-----QLIDNILESDIDRDGTIN 169
 DB 112 GNGYISRSEMEIYQAI-----YKMVSSVMKPEDESTPEKRTDKIFROMDINNKGKLS 165
 QY 170 LSEF-----QHVISRSPDFASSF 187
 DB 166 LEEFIKAKSDPSIVRLQCDPSSASQF 193

RESULT 14
 US-09-258-016-3
 Sequence 3, Application US/09258016
 Patent No. 6362395
 GENERAL INFORMATION:
 APPLICANT: Bachettlira W. Poovalah, Zhinua Liu,
 APPLICANT: Shameekumar Patil, Daisuke Takezawa
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
 TITLE OF INVENTION: PRODUCTION OF MALE-STERILE PLANTS
 NUMBER OF SEQUENCES: 19
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Klariquist Sparkman Campbell Leigh &
 ADDRESSEE: Whinston, LLP
 STREET: One World Trade Center
 STREET: 121 S.W. Salmon Street
 STREET: Suite 1600
 CITY: Portland
 STATE: Oregon
 COUNTRY: United States of America
 ZIP: 97204
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Disk, 3-1/2 inch
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: MS DOS
 SOFTWARE: Wordperfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/258,016
 FILING DATE:
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Stephens Jr., Donald L.

REGISTRATION NUMBER: 34,022
 REFERENCE/DOCKET NUMBER: 4630-51994
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (503) 226-7391
 TELEFAX: (503) 228-9446
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 193 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 DESCRIPTION: Region of rat neural vlslnln-like protein
 DESCRIPTION: (Gen2:Ratnvp3) with homology to lily
 DESCRIPTION: CCAMK
 US-09-258-016-3

Query Match 15.4%; Score 147; DB 4; Length 193;
 Best Local Similarity 24.5%; Pred. No. 9.7e-09;
 Matches 51; Conservative 41; Mismatches 80; Indels 36; Gaps 7;

QY 1 MGGSGRLSKELLAAYQDLFLTKQELLAHRRCELLPQEQRTVESSLRAQVFEQILS 60
 DB 1 MGKQNSKLRPEVLQDLREHTEFTDHELQEWYKGLKDCPTGHLTYDE-----FKKIYA 53
 QY 61 --LPELKANPEKERICRVSTSPAKDSLSFEFLLSVFSDTATPDIKSHYAFRIFFD 118
 DB 54 NFFPYGDAKFAEHVFTFDIN-SDGTIDFREFIALLSVTS-RGKLEQIKWAFSMYDLD 111
 QY 119 DDGTLNREXLSRLVNLGEGEDTRLASASEM-----QLIDNILESDIDRDGTIN 169
 DB 112 GNGYISRSEMEIYQAI-----YKMVSSVMKPEDESTPEKRTDKIFROMDINNKGKLS 165
 QY 170 LSEF-----QHVISRSPDFASSF 187
 DB 166 LEEFIKAKSDPSIVRLQCDPSSASQF 193

RESULT 15
 US-09-257-825B-3
 Sequence 3, Application US/09257825B
 Patent No. 6403352
 GENERAL INFORMATION:
 APPLICANT: Poovalah, Bachettlira W.
 APPLICANT: Patil, Shameekumar
 APPLICANT: Takezawa, Daisuke
 TITLE OF INVENTION: Compositions and Methods for Production of Male-Sterile Plan
 FILE REFERENCE: 4630-51993
 CURRENT APPLICATION NUMBER: US/09/257,825B
 PRIOR FILING DATE: 1999-02-25
 PRIOR APPLICATION NUMBER: US 08/655,352
 PRIOR FILING DATE: 1996-05-23
 PRIOR APPLICATION NUMBER: US 60/014,743
 NUMBER OF SEQ ID NOS: 28
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 3
 LENGTH: 193
 TYPE: PRT
 ORGANISM: Rat
 US-09-257-825B-3

Query Match 15.4%; Score 147; DB 4; Length 193;
 Best Local Similarity 24.5%; Pred. No. 9.7e-09;
 Matches 51; Conservative 41; Mismatches 80; Indels 36; Gaps 7;

QY 1 MGGSGRLSKELLAAYQDLFLTKQELLAHRRCELLPQEQRTVESSLRAQVFEQILS 60
 DB 1 MGKQNSKLRPEVLQDLREHTEFTDHELQEWYKGLKDCPTGHLTYDE-----FKKIYA 53
 QY 61 --LPELKANPEKERICRVSTSPAKDSLSFEFLLSVFSDTATPDIKSHYAFRIFFD 118
 DB 54 NFFPYGDAKFAEHVFTFDIN-SDGTIDFREFIALLSVTS-RGKLEQIKWAFSMYDLD 111

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 17, 2003, 12:46:59 ; Search time 31 Seconds
(without alignments)
1269.516 Million cell updates/sec

Title: MUT127
Perfect score: 957
Sequence: 1 MGSGSRLSKELLAETDLDL.....EFQHVISRSPDPASSFKIVL 191

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	408	42.6	311	5 Q93640	Q93640 caenorhabd1
2	364	38.0	185	11 Q9D9N5	Q9d9n5 mus musculu
3	341	35.6	187	4 Q96Q77	Q96q77 homo sapien
4	338.5	35.4	206	5 Q9W2O5	Q9w2q5 drosophila
5	272	28.4	54	6 Q9GLJ2	Q9glj2 sus scrofa
6	226.5	23.7	180	5 Q9GP83	Q9gp83 dictyostel
7	201	21.0	175	5 Q9UOX7	Q9uox7 leishmania
8	189	19.7	175	10 Q9LS47	Q9ls47 arabidopsis
9	188	19.6	175	10 Q93VF2	Q93vf2 eucalyptus
10	183.5	19.2	169	5 Q9NFN1	Q9nfn1 schistosoma
11	182.5	19.1	244	5 Q2O8O4	Q2o8o4 caenorhabd1
12	181.5	19.0	189	5 Q9VNF9	Q9vnf9 drosophila
13	179.5	18.8	170	5 Q9NKM7	Q9nkw7 patinopecte
14	179.5	18.8	170	5 Q95P81	Q95p81 bombyx mori
15	178	18.6	200	5 Q8SRF8	Q8srf8 encephalito
16	176.5	18.4	115	11 Q99LO9	Q99lq9 mus musculu

17	175.5	18.3	187	5 Q9VWX8	Q9vwx8 drosophila
18	170.5	17.8	175	3 Q9HDE1	Q9hde1 cryptococcu
19	170.5	17.8	177	3 Q9HDD3	Q9hdd3 cryptococcu
20	170	17.8	274	10 Q9AWM4	Q9aww4 oryza sativ
21	169.5	17.7	195	5 Q23643	Q23643 caenorhabd1
22	169.5	17.7	213	5 Q16343	Q16343 caenorhabd1
23	169.5	17.7	213	10 Q9LTB8	Q9ltb8 arabidopsis
24	169	17.7	170	4 Q8WYJ4	Q8wyj4 homo sapien
25	169	17.7	173	4 Q96LZ3	Q96l23 homo sapien
26	169	17.7	190	5 Q9NAY9	Q9nay9 naegleria f
27	164.5	17.2	161	10 Q9AY39	Q9ay39 oryza sativ
28	163.5	17.1	226	10 Q81446	Q81446 arabidopsis
29	158	16.5	190	3 Q96X50	Q96x50 magnaporthe
30	158	16.5	190	3 Q8TGC0	Q8tgc0 magnaporthe
31	153	16.0	196	5 Q9N2Y1	Q9n2y1 caenorhabd1
32	153	16.0	225	10 Q8W5C8	Q8w5c8 oryza sativ
33	151.5	15.8	226	10 Q81447	Q81447 arabidopsis
34	150.5	15.7	213	10 Q81445	Q81445 arabidopsis
35	150	15.7	246	10 Q82641	Q82641 arabidopsis
36	147	15.4	192	10 Q81328	Q81328 arabidopsis
37	147	15.4	222	10 Q81223	Q81223 arabidopsis
38	145	15.2	191	4 Q9UM19	Q9um19 homo sapien
39	141.5	14.8	153	5 Q9U5J0	Q9u5j0 trichomonas
40	141.5	14.8	160	5 Q9U5I9	Q9u5i9 trichomonas
41	140	14.6	29	11 Q99JY5	Q99jy5 mus musculu
42	137	14.3	216	11 Q9J557	Q9j557 mus musculu
43	137	14.3	220	4 Q9NS60	Q9ns60 homo sapien
44	137	14.3	220	4 Q9HD11	Q9hd11 homo sapien
45	137	14.3	220	11 Q9Jm60	Q9j60 rattus norv

ALIGNMENTS

RESULT 1	
Q93640	PRELIMINARY; PRT; 311 AA.
ID Q93640	
AC Q93640;	
DT 01-FEB-1997 (TREMBLrel. 02, Created)	
DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)	
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)	
DE F30A10.1 protein.	
GN F30A10.1.	
OS Caenorhabditis elegans.	
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;	
OC Rhabditidae; Peloderinae; Caenorhabditis.	
OX NCBI_TaxID=6239;	
RN [1]	
RP SEQUENCE FROM N.A.	
RA Barlow K.;	
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.	
RN [2]	
RP SEQUENCE FROM N.A.	
RX MEDLINE=99069613; PubMed=9851916;	
RA none;	
RT "Genome sequence of the nematode C.elegans: A platform for	
RT investigating biology.";	
RL Science 282:2012-2018(1998).	
DR EMBL; Z81072; CAB03019.1; -.	
DR HSSP; Q99828; IDGV.	
DR InterPro; IPR002048; EF-hand.	
DR Pfam; PF00036; ehand; 3.	
DR ProDom; PD000012; EF-hand; 1.	
DR SMART; SM00054; Efh; 2.	
SQ SEQUENCE 311 AA; 35960 MW; 97AF0AF56A6F526F CRC64;	
Query Match 42.6%; Score 408; DB 5; Length 311;	
Best Local Similarity 42.0%; Pred. No. 1.2e-27;	
Matches 87; Conservative 42; Mismatches 52; Indels 26; Gaps 5;	
OY 1 MGSGSRLS-----KELLAETDLDLFLTKQETLLAHRFCCELLPQEQRTVESS 48	
Db 111 MGNNASSLSLSENLFSKGVFTREQLDEYQDCTFFTRKDIIRLYKRYALNPHK---VPTN 167	


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RC STRAIN-BERKELEY;
RX MEDLINE-20196006; PubMed-10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abriil J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Bailew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Broksteln P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downe M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriere S., Fleischmann W.,
RA Foslter C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclebo J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svrtskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissensbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
DR EMBL; AE003452; AAF46635.1; -.
DR HSSP; Q99828; 1DGV.
DR FLYBase; FBgn0034558; CG9236.
DR InterPro; IPR002048; EF-hand.
DR Pfam; PF00036; efhand; 3.
DR ProDom; PD000012; EF-hand; 1.
DR SMART; SM00054; EFh; 3.
DR PROSITE; PS00018; EF_HAND; 2.
KW Calcium-binding.
SQ SEQUENCE 206 AA; 23591 MW; B3105F770F475A9 CRC64;

Query Match 35.4%; Score 338.5; DB 5; Length 206;
Best Local Similarity 43.8%; Pred. No. 8.2e-22;
Matches 77; Conservative 31; Mismatches 51; Indels 17; Gaps 5;

QY 17 QDLFLTKQELILAHRRFCCELLPQ--EQRTVSSSLRAQVPFEQILSLPELKNPFKERI 73
DB 43 KDCFTFTRKELIRVHKRFRELRLPDLVPRQMTGQASSVKVPCCEIEKMPELR----- 94

QY 74 CRVFSTSPAKDLSLSEFEDFLDLVSFSDATFPDIKSHYAFRIFFEDDDGTINEXLSRLVN 133
DB 95 -EAFSRD-GCGNLSFEFDLALSVSEQAPRDIKVFYAFKIYDFDQDGFIGHAD---LMS 149

QY 134 CLTGEGETRLASASEMKQLIDNILESDIDRDGTINLSEFQHVISRSPDFASSFKI 189
DB 150 CLTMTMKN-ELSPBEHQIADKVIIEADVDGDKLSILEFEHVILRAPDLSTFHI 204

RESULT 5
ID Q9GLJ2 PRELIMINARY; PRT; 54 AA.
AC Q9GLJ2;
DT 01-MAR-2001 (Tremblrel. 16, Created)
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DT 01-MAR-2001 (Tremblrel. 16, last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, last annotation update)
DE DNA-PK interaction-like protein (Fragment).
OS Sus scrofa (pig).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Smith T.P.L., Fahrenkrug S.C., Rohrer G.A., Simmen F.A.,
RA Rexroad C.E. III, Keele J.W.;
RT "Mapping of Expressed Sequence Tags from a porcine early embryonic
RT cDNA library."
RL Submitted (May-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF267715; AAG25931.1; -.
DR HSSP; Q99828; 1DGV.
DR InterPro; IPR002048; EF-hand.
DR Pfam; PF00036; efhand; 1.
DR ProDom; PD000012; EF-hand; 1.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
FT NON_TER 1
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 54 AA; 6107 MW; 1A8057DE68A57A4A CRC64;

Query Match 28.4%; Score 272; DB 6; Length 54;
Best Local Similarity 96.3%; Pred. No. 8.9e-17;
Matches 52; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 102 ATPDIKSHYAFRIFFDDGTLNREXISRVLNCLTGEGETRLASASEMKQLIDN 155
DB 1 ATPDIKSHYAFRIFFDDGTLNREXISRVLNCLTGEGETRLASASEMKQLIDN 54

RESULT 6
ID Q9GP83 PRELIMINARY; PRT; 180 AA.
AC Q9GP83;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-JUN-2001 (Tremblrel. 17, last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, last annotation update)
DE Calciineurin B.
GN CNBA.
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyostellida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-AX-2;
RA Alchem A.;
RL Thesis (2000), Department of Fachbereich Biologie,
RL Universitaet Konstanz, Konstanz, Germany.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-AX-2;
RA Alchem A.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ301668; CAC20026.2; -.
DR HSSP; P06705; 1AUI.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR001125; Recoverin.
DR Pfam; PF00036; efhand; 4.
DR PRINTS; PR00450; RECOVERIN.
DR ProDom; PD000012; EF-hand; 2.
DR SMART; SM00054; EFh; 4.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_3.
SQ SEQUENCE 180 AA; 20739 MW; E2E947E8D280D0B6 CRC64;

Query Match 23.7%; Score 226.5; DB 5; Length 180;
Best Local Similarity 29.8%; Pred. No. 3.9e-12;
Matches 53; Conservative 44; Mismatches 66; Indels 15; Gaps 4;

QY 1 MGGSGSRLSKELIAEYQDLFLTKQELILAHRRFCCELLPQEQRTVSSSLRAQVPFEQILS 60
ID 1 MGGSGSRLSKELIAEYQDLFLTKQELILAHRRFCCELLPQEQRTVSSSLRAQVPFEQILS 60
AC 1 MGGSGSRLSKELIAEYQDLFLTKQELILAHRRFCCELLPQEQRTVSSSLRAQVPFEQILS 60
DT 01-MAR-2001 (Tremblrel. 16, Created)
```

Db 1 MGNQHSLLNKEQLEQMKDNSSFSAEALKKLYRRFQMLDKDGSGLTT-----DEFLS 52

QY 61 LPPELKANPFKERICRVFSTSPAKDS-LSFEDFLDLLSVFSDTATPDIKSHYAFRIFFDD 119

Db 53 IPDLALNPLLRVIQIFDQ--KONEIEFSEFVGTATLSHKGTKEDKLKFLFQIYDIDC 110

QY 120 DGTNLNREXLSRLVCLTGEGETRLSASEMKQLIDNILEESDIDRGTINLSEFQHV 177

Db 111 DGFISNGELFQVLKMMVG---TNLNDVQLQIIVDKTIIEGDYDKDGKISFDEFIHI 164

RESULT 7

Q9U0X7 PRELIMINARY; PRT; 175 AA.

AC Q9U0X7

DT 01-MAY-2000 (TReMBLrel. 13, Created)

DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)

DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)

DE Calcineurin subunit.

GN L7171.06.

OS Leishmania major.

OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.

OX NCBI_TaxID=5664;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=FRIEDLIN;

RA Tosato V., Bruschi C.V., Ivens A.C., Murphy L., Quail M.,

RA Rajandream M.A., Barrell B.G.;

RL Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=FRIEDLIN;

RX MEDLINE=98146435; PubMed=9477341;

RA Ivens A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M.,

RA Smith D.F.;

RA "A physical map of the Leishmania major Friedlin genome.";

RL Genome Res. 8:135-145(1998).

DR EMBL; AL133435; CAB62809.1; -.

DR HSSP; P06705; 1AUI.

DR InterPro; IPR002048; EF-hand.

DR InterPro; IPR001125; Recoverin.

DR Pfam; PF00036; ehand; 4.

DR PRINTS; PR00450; RECOVERIN.

DR PRODOM; PD000012; EF-hand; 2.

DR SMART; SM00054; EFh; 3.

DR PROSITE; PS00018; EF_HAND; UNKNOWN_2.

SQ SEQUENCE 175 AA; 19660 MW; 9448F127F4DFA0EB CRC64;

Query Match 21.0%; Score 201; DB 5; Length 175;

Best Local Similarity 25.3%; Pred. No. 6.3e-10;

Matches 46; Conservative 45; Mismatches 77; Indels 14; Gaps 4;

QY 8 LSKELLAEXQDLTFLTKQEILLAHRRFCELLPQEQTVESSLRAQVPFEQILSLPELKAN 67

Db 6 LTAEELQNIRESALTDAQVRLYKSFSL-----NKDKSGKITRAEFNSIPALASN 57

QY 68 PFKERICRVFSTSPAKDSLSFEDFLDLLSVFSDTATPDIKSHYAFRIFFDDGTINREX 127

Db 58 PLVDRVLAVMDTD-GDSTVDFGDFVRALAVLSSATSKEDKLRTFTKMYDVVDGGRISNKD 116

QY 128 LSRVNLCTGEGETRLSASEMKQLIDNILEESDIDRGTINLSEFQHVIRSPDFASSF 187

Db 117 LFQMLSIMVG---VNLSQLQIIVDKTIIEADVDRDGYITFEFQ-ALAVNSDFGDR 171

QY 188 KI 189

Db 172 NL 173

RESULT 8

Q9LS47 PRELIMINARY; PRT; 175 AA.

ID Q9LS47

AC Q9LS47;

DT 01-OCT-2000 (TReMBLrel. 15, Created)

DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)

DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)

DE Calcineurin b subunit (Protein phosphatase 2b regulatory subunit)-like

DE protein (Hypothetical 20.0 kDa protein).

GN AT3G18430.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.

OX NCBI_TaxID=3702;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=COLUMBIA;

RA Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata S.;

RL Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=COLUMBIA;

RX MEDLINE=20277480; PubMed=10819329;

RA Nakamura Y.;

RT "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence

RT features of the regions of 4,504,864 bp covered by sixty P1 and TAC

RT clones.";

RL DNA Res. 7:131-135(2000).

RN [3]

RP SEQUENCE FROM N.A.

RA Yamada K., Banh J., Banno F., Chang E., Dale J.M., Goldsmith A.D.,

RA Lee J.M., Onodera C.S., Quach H.L., Tang C., Toriumi M., Wu H.C.,

RA Yamamura Y., Yu G., Yu S., Bowser L., Carninci P., Chen H., Cheuk R.,

RA Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,

RA Kawai J., Kim C., Koesema E., Lam B., Lin J., Meyers M.C., Miranda M.,

RA Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M.,

RA Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,

RA Theologis A.;

RT "Full Length cDNA of gene At3g18430 (GI:15229640).";

RL Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.

RN [4]

RP SEQUENCE FROM N.A.

RA Yamada K., Banh J., Chan M.M., Chang C.H., Chang E., Dale J.M.,

RA Deng J.M., Goldsmith A.D., Lee J.M., Onodera C.S., Quach H.L.,

RA Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bowser L.,

RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,

RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,

RA Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J.,

RA Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Shinozaki K.,

RA Davis R.W., Ecker J.R., Theologis A.;

RT "Arabidopsis Open Reading Frame (ORF) Clones.";

RL Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.

DR EMBL; AB026658; BAB01109.1; -.

DR EMBL; AY063789; AAL36096.1; -.

DR EMBL; AY091287; AAM14226.1; -.

DR HSSP; P06705; 1AUI.

DR InterPro; IPR002048; EF-hand.

DR Pfam; PF00036; ehand; 2.

DR PRODOM; PD000012; EF-hand; 1.

DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.

KW Hypothetical protein.

SQ SEQUENCE 175 AA; 20032 MW; B26D6F2ADA26AFED CRC64;

Query Match 19.7%; Score 189; DB 10; Length 175;

Best Local Similarity 26.6%; Pred. No. 7e-09;

Matches 49; Conservative 46; Mismatches 65; Indels 24; Gaps 5;

QY 1 MGGSGSRLSKELLAEQYQ----DLTFLTKQEILLAHRRFCELLPQEQTVESSLRAQVPFE 56

Db 1 MGMTSSMLTQYDIEEVQSHCHDL--FEQQEILSLYQRFCDL-----DRNAKGFIAD 50

QY 57 QILSLPELKANPFKERICRVFSTSPAKDSLSFEDFLDLLSVFSDTATPDIKSHYAFRIFD 116

Db 51 EFLSVPEFAMNPLSQLLLKMV-----DGLNFKDFVAFLSAFSAKASLRQKVLIFKVD 104

QY 117 FDDDGTLNREXLSRLVCLTGEGETRLSASEMKQLIDNILEESDIDRGTINLSEFQHV 176

Db 75 GADASLPMECSNFDAYELRLT-----RRFKKL-----DVDGS--GSLSVPEEMS 118

QY 61 LPPELQNPVQVVIDIFD-EDGNGEVDFREFIQISQFSVKGDKNTKLKFAFRIYDMRD 177

Db 119 LPELQNPVQVVIDIFD-EDGNGEVDFREFIQISQFSVKGDKNTKLKFAFRIYDMRD 177

QY 121 GTLNREXSLVNLCTGEGEDTRLSASEMKQLIDNILEESIDRDGTINLSEFQHVISRS 180

Db 178 GFISNGELFQVLKMMVG-----NNLKDSQLQIYDKTILFHDKDGDKISFQECFVVEHT 233

RESULT 12

Q9VNF9 PRELIMINARY; PRT; 189 AA.

AC Q9VNF9;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)

DE CG2185 protein (LD19356p).

GN CG2185.

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI_TaxID=7227;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-BERKELEY;

RX MEDLINE=20196006; PubMed=10731132;

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Ananatzides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,

RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,

RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,

RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,

RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,

RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,

RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,

RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,

RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,

RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,

RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;

RT "The genome sequence of Drosophila melanogaster.";

RL Science 287:2185-2195(2000).

RN [2]

RN SEQUENCE FROM N.A.

RP STRAIN-BERKELEY;

RC STRAIN-BERKELEY;

RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,

RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,

RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,

RA Nunoo J., Pacleb J., Paragas V., Park S., Phouanavong S., Wan K.,

RA Yu C., Lewis S.E., Rubin G.M., Celniker S.;

RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AE003602; AAF51977.1; -.

DR EMBL; AY069465; AAL39610.1; -.

DR HSSP; P06705; IAU1.

DR FlyBase; FBgn0037358; CG2185.

DR InterPro; IPR002048; EF-hand.

DR Pfam; PF00036; ehand; 2.

DR ProDom; PD000012; EF-hand; 2.

DR SMART; SM00054; EFh; 2.

DR PROSITE; PS00018; EF_HAND; 1.

KW Calcium-binding.

SQ SEQUENCE 189 AA; 21996 MW; 3621BAF72BED845D CRC64;

Query Match 19.0%; Score 181.5; DB 5; Length 189;

Best Local Similarity 25.4%; Pred. No. 3.5e-08;

Matches 48; Conservative 42; Mismatches 78; Indels 21; Gaps 4;

QY 1 MGGSGSR-LSKELLAEQDLTFLTKQEIILAHRRFCELLPQEQRTVSESLRAQVPFEQIL 59

Db 1 MGNKSLFLRNEEIAQIQEETGFTPNQIERLYSRFTSLDRNDCGTLR-----EDLM 52

QY 60 SLPELKANPFKERICRVFSTSPAKDSLSFEEDFLDLLSVF-----SDTATPDIKSHYA 111

Db 53 RIPELAINPLCERIVHSFFAESNDRVNFQFMNVLAHFRPLRDNKQSKLSREKLFKA 112

QY 112 FRIEFDGDTLNREXSLVNLCTGEGEDTRLSASEMKQLIDNILEESIDRDGTINLS 171

Db 113 FKMYDLDDGVISRDELLSILHMMVG----ANISQQLVLSIAERTILEADLCCQKISFE 168

QY 172 EFQHVISRS 180.

Db 169 DFCKALDRT 177

RESULT 13

Q9NKKW7 PRELIMINARY; PRT; 170 AA.

AC Q9NKKW7;

DT 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)

DE Calcineurin B.

OS Patinopecten yessoensis (Ezo giant scallop) (Yesso scallop).

OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Pectinoidea;

OC Pectinoidea; Pectinidae; Mizuhopecten.

OX NCBI_TaxID=6573;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=TESTIS;

RA Uryu M., Nakatomi A., Watanabe M., Hatsuse R., Yazawa M.;

RT "Molecular Cloning of cDNA Encoding Two Subunits of Calcineurin from

RT Scallop Testis: Demonstration of Stage-Specific Expression during

RT Maturation of the Testis.";

RL J. Biochem. 0:0-0(2000).

DR EMBL; AB041524; BAA94543.1; -.

DR HSSP; P06705; IAU1.

DR InterPro; IPR002048; EF-hand.

DR InterPro; IPR001125; Recoverin.

DR Pfam; PF00036; ehand; 4.

DR PRINTS; PR00450; RECOVERIN.

DR ProDom; PD000012; EF-hand; 2.

DR SMART; SM00054; EFh; 4.

DR PROSITE; PS00018; EF_HAND; UNKNOWN_4.

SQ SEQUENCE 170 AA; 19238 MW; 9450322698470F44 CRC64;

Query Match 18.8%; Score 179.5; DB 5; Length 170;

Best Local Similarity 25.1%; Pred. No. 4.6e-08;

Matches 44; Conservative 42; Mismatches 70; Indels 19; Gaps 4;

QY 3 GSGSRLSKELLAEQDLTFLTKQEIILAHRRFCELLPQEQRTVSESLRAQVPFEQILSLP 62

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Db      2 GNENSLPMEICSNFD-----PDEIKRLGKRF-----RKLDLDSGSLSYDEMTLP 47
QY      63 ELKANPFKERICRVSTSPAKDSLSEFEDFLDLSVSDTATPDIKSHYAFRIFFDDGT 122
      48 ELQONPLVQVRVIDFDTD-NGEVEDFKEFIEGVSQFSVGDKLSKLRFAFRITYDMDKDGY 106
QY      123 LNREXLSRLVNCITGEGEDTRLASASEMKOLIDNILEESDIDRDGTINLSEFOHVI 177
      107 ISNGELFOVLKMMVG----NNLKDTQLQIYDKTIHADADGDGKISFEFCVAVV 157

RESULT 14
Q95P81  PRELIMINARY; PRT; 170 AA.
AC      Q95P81;
DT      01-DEC-2001 (Tremblrel. 19, last sequence update)
DT      01-DEC-2001 (Tremblrel. 19, last sequence update)
DT      01-MAR-2002 (Tremblrel. 20, last annotation update)
DE      Calcineurin B.
GN      CNB.
OS      Bombyx mori (Silk moth).
OC      Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC      Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC      Bombycoidea; Bombycidae; Bombyx.
OX      NCBI_TaxID=7091;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=SHUKO X RYUHAU; TISSUE=PEROMONE GLAND;
RA      Yoshiga T., Matsumoto S.;
RT      "CDNA cloning of heterosubunits of calcineurin from pheromone gland of
RT      Bombyx mori.";
RL      Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AF287251; AAK83039.1;
DR      InterPro; IPR002048; EF-hand.
DR      Pfam; PF00036; efhand; 4.
DR      ProDom; PD000012; EF-hand; 2.
DR      ProSITE; PS00018; EF_HAND; UNKNOWN_4.
SQ      SEQUENCE 170 AA; 19357 MW; 5ECC15B820097130 CRC64;

Query Match      18.8%; Score 179.5; DB 5; Length 170;
Best Local Similarity 24.7%; Pred. No. 4.6e-08;
Matches 44; Conservative 44; Mismatches 71; Indels 19; Gaps 4;

QY      3 GSGSRLSKELLAAYODLFLTKQELLHRRFCCELLPQEQRTVESSLRAQVPFEQILSLP 62
      2 GNENSIPMEICSNFD-----ADEIRRLGKRF-----RKLDLDSGSLSIDEFMSLP 47
QY      63 ELKANPFKERICRVSTSPAKDSLSEFEDFLDLSVSDTATPDIKSHYAFRIFFDDGT 122
      48 ELQONPLVQVRVIDFD-ADNGEVEDFKEFIEGVSQFSVGDKLSKLRFAFRITYDMDKDGF 106
QY      123 LNREXLSRLVNCITGEGEDTRLASASEMKOLIDNILEESDIDRDGTINLSEFOHVISRS 180
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DT      01-JUN-2002 (Tremblrel. 21, Created)
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DT      01-JUN-2002 (Tremblrel. 21, last sequence update)
DE      Calcineurin beta subunit.
GN      ECU08_0160.
OS      Encephalitozoon cuniculi.
OC      Eukaryota; Microsporidia; Unikaryonidae; Encephalitozoon.
OX      NCBI_TaxID=6035;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=GB-M1;
RA      Genoscope;
RL      Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.

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RN      [2]
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RC      STRAIN=GB-M1;
RX      MEDLINE=21576510; PubMed=11719806;
RA      Katinka M.D., Duprat S., Cornilliot E., Metenier G., Thomarat F.,
RA      Prensler G., Barbe V., Peyretailade E., Brotlier P., Winkler P.,
RA      Delbac F., El Alaoui H., Peyret P., Saurin W., Gouy M.,
RA      Weissenbach J., Vivares C.P.;
RT      "Genome sequence and gene compaction of the eukaryote parasite
RT      Encephalitozoon cuniculi.";
RL      Nature 414:450-453(2001).
DR      EMBL; AL590448; CAD26322.1;
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QY      120 DGTLNREXLSRLVNCITGEGEDTRLASASEMKOLIDNILEESDIDRDGTINLSEFOHVISR 179
      113 DGRLCRNVLIRINKMM---GQDGRVEEAE-----NLNLYDEGKGIDISDFTRYES 163
QY      180 SP-----DEASSFK 188
      164 DPLIDKNMIDFSKNLK 180

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Search completed: January 17, 2003, 12:49:11
Job time : 32 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 17, 2003, 12:46:44 ; Search time 36 Seconds
(without alignments)
706.969 Million cell updates/sec

Title: MUTL27
Perfect score: 957
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Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	374	39.1	172	22	AAU87324
5	374	39.1	184	22	AAW43562
6	372	38.9	185	22	AAW64418
7	348	36.4	173	22	ABB96054
8	348	36.4	173	22	AAU87612
9	348	36.4	173	22	AAW95362
10	348	36.4	173	22	AAW43637

11	348	36.4	173	22	AAU19952
12	340	35.5	187	22	AAE09736
13	338.5	35.4	206	22	ABB64325
14	239.5	25.0	169	23	ABP41194
15	217	22.7	120	20	AAV11976
16	203.5	21.3	175	20	AAV00881
17	190	19.9	175	21	AAW21178
18	190	19.9	210	21	AAW21177
19	189	19.7	175	21	AAW51586
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21	187	19.5	175	21	AAW07824
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23	185.5	19.4	170	21	AAW09978
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26	178	18.6	169	21	AAW07825
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38	169	17.7	189	22	AAW95239
39	169	17.7	189	22	AAW43564
40	169	17.7	189	22	AAW43639
41	169	17.7	189	22	AAU19951
42	163.5	17.1	226	21	AAW47032
43	162.5	17.0	226	21	AAW21763
44	156	16.3	190	21	AAW69996
45	155	16.2	194	22	AAU87585

ALIGNMENTS

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Drosophila melanog
Human ovarian anti
Human 5' EST seque
Calcineurin regula
Zea mays protein f
Zea mays protein f
Arabidopsis thalia
Herbicidally activ
Arabidopsis thalia
Human calcineurin.
Human HCNB protein
Drosophila melanog
Arabidopsis thalia
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Amino acid sequenc
Novel central nerv
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RESULT 1	AAW51215	standard; Protein; 191 AA.
AC	AAW51215;	
DT	21-AUG-1998	(first entry)
DE	Amino acid sequence of the calcium-integrin binding protein.	
KW	Human calcium-integrin binding protein; CIB; integrin alpha IIb;	
KW	cytoplasmic domain; platelet; alpha IIB-beta-3; fibrinogen receptor;	
KW	Inhibition; blood coagulation; vascular disorder.	
OS	Homo sapiens.	
FH	Key	Location/Qualifiers
FT	Region	116..128
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FT	Region	160..173
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PN	WO9814471-A1.	
PD	09-APR-1998.	
PF	24-SEP-1997;	97WO-US16828.
PR	02-OCT-1996;	96US-0720625.
PA	(UYNC-) UNIV NORTH CAROLINA.	
PI	Nalk UP, Parise LV;	

XX PN WO9826056-A1.
XX PD 18-JUN-1998.
XX PF 25-NOV-1997; 97WO-US21603.
XX PR 12-DEC-1996; 96US-0764563.
XX PA (INCY-) INCYTE PHARM INC.
XX PI Goli SK, Hillman JL;
XX DR WPI; 1998-348518/30.
XX DR N-PSDB; V398009.
PT New protein phosphatase regulatory sub-unit - useful for diagnosis,
PT prevention and treatment of immuno-suppression, neuro-degeneration,
PT inflammation and cancer
XX PS Claim 1; Fig 1; 65pp; English.
XX CC The present sequence is a pure human protein phosphatase regulatory
CC subunit (HCNB). Host cells, comprising a vector containing DNA encoding
CC HCNB, are used to produce recombinant HCNB which is used to treat or
CC prevent immunosuppression or neurological diseases (especially parasitic,
CC bacterial or viral infections, including AIDS; the effects of radio- or
CC chemo-therapy and Alzheimer's disease). Antagonists which bind
CC specifically to HCNB and modulate its activity are used to treat
CC inflammation, cancer, or immunological disorders and allograft rejection
CC (especially anaemia, asthma, systemic lupus erythematosus, myasthenia
CC gravis, diabetes, thyroiditis, ulcerative colitis, osteoporosis and
CC arthritis). Complements of the DNA encoding HCNB are useful as probes
CC and primers for detecting the DNA encoding HCNB by hybridisation or
CC amplification assays, while Ab can be used to detect HCNB by immunoassay,
CC particularly for diagnosis of the specified disorders, including early
CC diagnosis of cancers. The probes can also be used to map the
CC corresponding genomic sequence, while Ab are also useful in drug
CC screening and for purifying native HCNB. Therapeutic agents are
CC administered orally, intravenously, intramuscularly, topically or
CC rectally, normally at 0.1-105 mu g.
XX SQ Sequence 191 AA;
Query Match 97.0%; Score 928; DB 19; Length 191;
Best local Similarity 98.4%; Pred. No. 3.2e-89;
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DB 181 PDFASSFKIYL 191
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AAU87324
ID AAU87324 standard; Protein; 172 AA.
XX AC AAU87324;
XX DT 05-JUN-2002 (first entry)
XX

DE Novel central nervous system protein #234.
XX KW Central nervous system; CNS; autoimmune disease; rheumatoid arthritis;
KW hyperproliferative disorder; neoplasm; cardiovascular disorder;
KW cardiac arrest; cerebrovascular disorder; ischemia; angiogenesis;
KW nervous system disorder; Alzheimer's disease; AIDS; ocular disorder;
KW acquired immunodeficiency virus; dysphagia; gastrointestinal disorder;
KW adenocarcinoma; reproductive system disorder; testicular feminisation;
KW endocrine disorder; diabetes; cancer; leukaemia; neovascularisation;
KW respiratory disorder; renal disorder; kidney failure; blood disorder;
KW myocardial infarction; wound healing; cell proliferation; skin aging;
KW food additive; food preservative; gene therapy.
XX OS Homo sapiens.
XX PN WO200155318-A2.
XX PD 02-AUG-2001.
XX PF 17-JAN-2001; 2001WO-US01332.
XX PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
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PR 12-SEP-2000; 2000US-0231968.


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XX DE      Human polypeptide SEQ ID NO 240.
XX XX
KW Human; antiarthritic; antirheumatic; antiproliferative; vasotropic;
KW cerebroprotective; nootropic; neuroprotective; antibacterial; virucide;
KW fungicide; ophthalmological; cytostatic; immunosuppressive; nootropic;
KW neuroprotective; antiallergic; hepatotropic; antidiabetic;
KW antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial;
KW antiparasitic; cardiant; gene therapy; cancer; immune disorder;
KW cardiovascular disorder; neurological disease; infection; human.
XX
OS Homo sapiens.
XX
PN WO200155308-A2.
XX
PD
XX 02-AUG-2001.
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PF 17-JAN-2001; 2001WO-US01309.
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PR 05-JAN-2001; 2001US-0259678.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PI
PI Rosen CA, Barash SC, Ruben SM;
XX
DR WPI; 2001-488781/53.
DR N-PSDB; AAI63868.
XX
PT New isolated nucleic acids and polypeptides, useful for diagnosing,
PT treating and/or preventing human diseases and disorders -
XX
PS Claim 11; SEQ ID NO 240; 664pp + Sequence Listing; English.
XX
CC The invention relates to human polynucleotides (AAI63803-AAI64012) and
CC the encoded proteins (AAM434497-AAM43660) useful for preventing, treating
CC or ameliorating medical conditions e.g. by protein or gene therapy. The
CC genes were isolated from a range of human tissues disclosed in the
CC specification. The nucleic acids, proteins, antibodies and (ant)agonists
CC are useful in the diagnosis, treatment and prevention of: (a) cancer,
CC e.g. breast and ovarian cancer and other cancers of the adrenal gland,
CC bone, bone marrow, breast, gastrointestinal tract, liver, lung, or
CC urogenital; (b) immune disorders e.g. Addison's disease, allergies,
CC autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus,
CC Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative
CC colitis; (c) cardiovascular disorders such as myocardial ischaemias;
CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
CC and parasitic infections.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 184 AA;
Query Match 39.1%; Score 374; DB 22; Length 184;
Best Local Similarity 43.5%; Pred. No. 4.3e-31;
Matches 77; Conservative 37; Mismatches 53; Indels 10; Gaps 3;
QY 13 LAEYQDLTFLTKQEIILAHRRFCELLPQEQRTVSSSLRAQVPFEQILSLPELKANPFKE 72
Db 13 LEEYQALTFLTRNEILCIHDTFLKLCPPGKYKATL---TMDQVSSLPALRVNPFDR 68
QY 73 ICRVFTSPAKDSLSFEDFLDLLSVFSDTATPDIKSHYAFRIFDDDDGTNLNREXLSRLV 132
Db 69 ICRVFS---HKGMFSFEDVLGMASVFSEQAQPSLKIEYAFRIYDFNENGFIDEEDLQRII 125
QY 133 NCLTGEDETRLSASEMKQLIDNILEESDIDRDGTINLSEFQHVISRSPDFASFSKI 189
Db 126 LRLNSDD---MSEDLMLDTLTHVLSSEDLNDNMLSFSEFEHAKSPDFMNSFRI 179
RESULT 6
AAB64418
ID AAB64418 standard; Protein; 185 AA.
XX
AC AAB64418;
XX
DT 22-MAR-2001 (first entry)
XX
DE Amino acid sequence of human intracellular signalling molecule INTRA50.
XX
KW Human; intracellular signalling molecule; INTRA; immunosuppressive;
KW cytostatic; neuroprotective; nootropic; antiarteriosclerotic; cancer;
KW antiinflammatory; anti-HIV; neuroleptic; antibacterial; antifungal;

KW antiviral; antiparasitic; antihelminthic; antiparkinsonian; AIDS;
KW cell proliferative disorder; arteriosclerosis autoimmune; epilepsy;
KW inflammatory disorder; Addison's disease; gastrointestinal disorder;
KW neurological disorder; Parkinson's disease; Creutzfeldt-Jakob disease;
KW mental disorder; schizophrenia; anxiety.
XX
OS Homo sapiens.
XX
PN WO200077040-A2.
XX
PD 21-DEC-2000.
XX
PF 16-JUN-2000; 2000WO-US16636.
XX
PR 16-JUN-1999; 99US-0139566.
PR 17-AUG-1999; 99US-0149640.
PR 09-NOV-1999; 99US-0164417.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Yue H, Tang YT, Hillman JL, Lal P, Bandman O, Baughn MR;
PI Azimzai Y, Yang J, Reddy R, Lu DAM;
XX
DR WPI; 2001-025334/03.
DR N-PSDB; AAF32687.
XX
PT New human intracellular signalling molecules, useful for the diagnosis,
PT prevention and treatment of cell proliferative, autoimmune,
PT inflammatory, neurological, gastrointestinal, reproductive and
PT developmental disorders -
XX
PS Claim 5; Page 158-159; 192pp; English.
XX
CC Sequences AAF32638 - AAF32689 represent cDNA encoding human
CC intracellular signalling molecules INTRAL - INTRA52, represented in
CC AAB64369 - AAB64420. Modulators of the intracellular signalling molecules
CC of the invention exhibit immunosuppressive; cytostatic; neuroprotective;
CC nootropic; antiarteriosclerotic; antiinflammatory; anti-HIV;
CC neuroleptic; antibacterial; antifungal; antiviral; antiparasitic;
CC antihelminthic; and antiparkinsonian activity. INTRA polypeptides their
CC agonists and antagonists are useful for the treatment of a condition
CC associated with decreased or increased expression of functional INTRA.
CC Disorders associated with abnormal INTRA expression or activity include
CC cell proliferative disorders e.g. arteriosclerosis and cancers;
CC autoimmune or inflammatory disorders e.g. Addison's disease and acquired
CC immunodeficiency syndrome (AIDS); viral, bacterial, fungal, parasitic,
CC protozoal and helminthic infections; gastrointestinal disorders e.g.
CC dysphagia and irritable bowel syndrome; neurological disorders e.g.
CC epilepsy and Parkinson's disease; prion diseases e.g. Creutzfeldt-Jakob
CC disease and mental disorders e.g. anxiety, schizophrenia and Tourette's
CC disorder. Antibodies immuno specific for the INTRA proteins may also be
CC useful in the diagnosis of the above disorders.
XX
SQ Sequence 185 AA;
Query Match 38.9%; Score 372; DB 22; Length 185;
Best Local Similarity 43.6%; Pred. No. 7.1e-31;
Matches 78; Conservative 36; Mismatches 55; Indels 10; Gaps 3;
QY 11 ELLAEYQDLTFLTKQEIILAHRRFCELLPQEQRTVSSSLRAQVPFEQILSLPELKANPFK 70
Db 12 EDLEEYQALTFLTRNEILCIHDTFLKLCPPGKYKATL---TMDQVSSLPALRVNPF 67
QY 71 ERICRVFTSPAKDSLSFEDFLDLLSVFSDTATPDIKSHYAFRIFDDDDGTNLNREXLSR 130
Db 68 DRICRVFS---HKGMFSFEDVLGMASVFSEQAQPSLKIEYAFRIYDFNENGFIDEEDLOR 124
QY 131 LVNCLTGEDETRLSASEMKQLIDNILEESDIDRDGTINLSEFQHVISRSPDFASFSKI 189
Db 125 IILRLNSDD---MSEDLMLDTLTHVLSSEDLNDNMLSFSEFEHAKSPDFMYSFRI 180
RESULT 7

ABB96054
ID ABB96054 standard; Protein; 173 AA.
XX
AC ABB96054;
XX
DT 21-JUN-2002 (first entry)
XX
DE Human testicular antigen SEQ ID NO: 1438.
XX
KW Human; testicular antigen; testes; cancer; metastasis; immune disorder;
KW reproductive system disorder; urinary system disorder; gene therapy;
KW cardiovascular disorder; respiratory disorder; neurological disorder;
KW gastrointestinal disease; infection; cytostatic.
XX
OS Homo saplens.
XX
PN WO200155317-A2.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01329.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
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PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
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PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
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PR 18-AUG-2000; 2000US-0226279.
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PR 29-SEP-2000; 2000US-0236367.
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PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
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PR 20-OCT-2000; 2000US-0241785.
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PR 20-OCT-2000; 2000US-0241808.
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PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
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PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.

PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
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PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
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PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
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PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
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PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
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PR 08-NOV-2000; 2000US-0246609.
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PR 17-NOV-2000; 2000US-0249211.
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PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
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PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249266.
PR 17-NOV-2000; 2000US-0249267.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 11-DEC-2000; 2000US-0251990.
PR 05-JAN-2001; 2001US-0259678.
XX
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX

PI Rosen CA, Barash SC, Ruben SM;
XX
DR WPI; 2001-581633/65.
DR N-PSDB; ABK43942.
XX
PT New isolated nucleic acid encoding a protein for diagnosing,
PT preventing, treating or ameliorating medical conditions and used as
PT food additives or preservatives
XX
PS Claim 9; SEQ ID No 1130; 837pp; English.
XX
CC The invention describes an isolated nucleic acid molecule (I) encoding a
CC novel central nervous system protein. (I) and polypeptides (II) encoded
CC by (I), are used to treat a medical conditions and in diagnosis of a
CC pathological condition. Disorders which are diagnosed or treated include
CC autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative
CC disorders e.g. neoplasms of the breast or liver, cardiovascular disorders
CC e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia,
CC angiogenesis, nervous system disorders e.g. Alzheimer's disease and
CC amyotrophic lateral sclerosis, infections caused by bacteria, viruses
CC e.g. acquired immunodeficiency virus (AIDS) and fungi, ocular disorders
CC e.g. corneal infection, gastrointestinal disorders e.g. dysphagia,
CC adenocarcinomas and irritable bowel syndrome, reproductive system
CC disorders e.g. testicular feminisation, endocrine disorders e.g. diabetes
CC and pituitary dwarfism, cancers and disorders at the cellular level e.g.
CC leukaemia, disorders involving neovascularisation e.g. malignancies,
CC respiratory disorders e.g. nonallergic rhinitis, renal disorders e.g.
CC acute kidney failure and blood related disorders e.g. myocardial
CC infarction. The polypeptides can also be used to aid wound healing and
CC epithelial cell proliferation, to prevent skin aging due to sunburn, to
CC maintain organs before transplantation, for supporting cell culture of
CC primary tissues, to regenerate tissues and in chemotaxis. The
CC polypeptides can also be used as a food additive or preservative to
CC increase or decrease storage capabilities, fat content, lipid, protein,
Query Match 36.4%; Score 348; DB 22; length 173;
Best Local Similarity 42.3%; Pred. No. 2.1e-28;
Matches 74; Conservative 36; Mismatches 55; Indels 10; Gaps 3;
QY 13 LAEYQDLTFLTKQEIILAHRRCELLPQEQRTVESSLRAQVFEQILSLPELKANPEKER 72
Db 1 LEEYQALFTLTRENIILCIHDTFLKICPGKYKKEATL----TMDQVSSLPALRVNPFDR 56
QY 73 ICRVSTSPAKDSLFEDEFLDLSVSDTATPDIKSHYAFRIFFDDGTLNREXISRLV 132
Db 57 ICRVFS--HKGMFSFEDYLGMAVSFSEQACPSLKIEYAFRIYDFENNGFIDEDLQRII 113
QY 133 NCLTGEGETRLSASEMKQLIDNILEESDIDRGITINLSEFOHVISRSPDASSF 187
Db 114 LRLNSDD---MSEDLMDLTNHYLSXSDLDNDNMLSESEFEHAMAKSPDMTPF 165
RESULT 9
AAM95362
ID AAM95362 standard; Protein; 173 AA.
XX
AC AAM95362;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human reproductive system related antigen SEQ ID NO: 4020.
XX
KW Human; reproductive system related antigen; reproductive system disorder;
KW cancer; gene therapy.
XX
OS Homo sapiens.
XX
PN WO200155320-A2.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01339.
XX

PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184564.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
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PR 14-AUG-2000; 2000US-0224519.
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PR 01-SEP-2000; 2000US-0229287.
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PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
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PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
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PR 17-NOV-2000; 2000US-0249244.
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PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.

(HUMA-) HUMAN GENOME SCI INC.
Rosen CA, Barash SC, Ruben SM;
WPI; 2001-465570/50.
N-PSDB; AAL01332.
Isolated nucleic acid molecule encoding a reproductive system antigen
is used in preventing, treating or ameliorating a medical condition -

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PI
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DR
DR
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PT

XX PS Claim 11; SEQ ID NO 4020; 1297pp + Sequence Listing; English.
XX CC The present invention provides the protein and coding sequences of a
CC number of human reproductive system related antigens. These can be used
CC in the prevention and treatment of reproductive system disorders,
CC including cancer. The present sequence is a protein of the invention.
XX
SQ Sequence 173 AA;

Query Match 36.48; Score 348; DB 22; Length 173;
Best Local Similarity 42.38; Pred. No. 2.1e-28;
Matches 74; Conservative 36; Mismatches 55; Indels 10; Gaps 3;

OY 13 LAEYQDLFLTKQELLAHRCCELLPQEQRTVESSLRAQVPEQILSLPELKNPFKER 72
Db 1 LEEYQALFLTRNEILCHDTFLKLCPPGKYKEATL---TMDQVSLPALRVNPFDR 56
OY 73 ICRVSTSPAKDSLSEFEDFLDLLSVESDTATPDIKSHYAFRIEFDGTLNREXSLRV 132
Db 57 ICRVFS--HKGFSEFDVLGMASVFSEQACPSLKIEYAFRIYDFNENGFIDEEDLORII 113
OY 133 NCLTGEGEDTRLSASEMKOLIDNILEESDIDRDGTINLSEFQHVISRSPDFASSF 187
Db 114 LRLNSDD---MSEDLMDLTNHLVLSXSDLDNDNMLSEFSEFHAMAKSPDWTPTF 165

RESULT 10

AAM43637
ID AAM43637 standard; Protein; 173 AA.
XX
AC AAM43637;

DT 22-OCT-2001 (first entry)
XX
DE Human polypeptide SEQ ID NO 315.

XX Human: antiarthritic; antirheumatic; antiproliferative; vasotropic;
KW cerebroprotective; nootropic; neuroprotective; antibacterial; virucide;
KW fungicide; ophthalmological; cytostatic; immunosuppressive; nootropic;
KW neuroprotective; antiallergic; hepatotropic; antidiabetic;
KW antiinflammatory; antiulcer; vulnary; anticonvulsant; antibacterial;
KW antiparasitic; cardiant; gene therapy; cancer; immune disorder;
KW cardiovascular disorder; neurological disease; infection; human.
XX
OS Homo sapiens.

PN NO200155308-A2.

PD 02-AUG-2001.

PF 17-JAN-2001; 2001WO-US01309.

XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
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PR 19-MAY-2000; 2000US-0205515.
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PR 21-SEP-2000; 2000US-0234274.
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 PR 08-DEC-2000; 2000US-0251869.
 PR 08-DEC-2000; 2000US-0251989.
 PR 11-DEC-2000; 2000US-0251990.
 PR 05-JAN-2001; 2001US-0259678.

(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Barash SC, Ruben SM;

WPI; 2001-465568/50.

N-PSDB; AAS31637.

Isolated nucleic acid molecule encoding a calcium-binding protein is used in preventing, treating or ameliorating a medical condition -

Claim 11; SEQ ID No 149; 542pp; English.

The present invention relates to the isolation of novel human calcium-binding proteins, and cDNA (AAS31577-AAS31654) and genomic sequences encoding for these proteins. The sequences of the invention are useful in the diagnosis, prevention and/or prognosis of diseases associated with aberrant calcium flux. Such disorders include CC neurological diseases (e.g. amyotrophic lateral sclerosis, ALS), CC immune dysfunction (e.g. severe combined immunodeficiency, SCID), CC digestive disorders (e.g. irritable bowel syndrome, IBS), neoplastic disease (e.g. cancer), blood disorders (e.g. haemophilia), and/or CC infectious disease (e.g. acquired immunodeficiency syndrome, AIDS). The novel calcium-binding proteins are also useful as screening tools to CC identify antagonists and/or agonists that may enhance or inhibit CC activities mediated by calcium-binding proteins. The polynucleotides of CC the invention are also useful in gene therapy. AAU19892-AAU19969 CC represent the novel human calcium-binding proteins.
 CC Note: The sequence data for this patent did not form part of the printed CC specification, but was obtained in electronic format directly from WIPO CC at ftp.wipo.int/pub/published_pct_sequences.
 CC XX

Sequence 173 AA;

Query Match 36.4%; Score 348; DB 22; Length 173;
 Best Local Similarity 42.3%; Pred. No. 2.1e-28;
 Matches 74; Conservative 36; Mismatches 55; Indels 10; Gaps 3;

Db 43 KDCFTETREILRVHKKRRELRLPDLVPRQMTGQASSVKVPCCECIEMPELR----- 94
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Db 95 -EAFSRD-CGQNLSEFEDFLDALSVSEQAAPRDIKVFYAFKIYDFDQDGFIGHAD--LMS 149
QY 134 CLTGEEDTRLASASEMKQOLIDNILEESDIDRDGTINLSEFOHVISRSPDEASSFKI 189
Db 150 CLTTMTKN-ELSPEEHQIADKYIEADVDDGDKLSILEFEHVILRAPDFLSTFHI 204
RESULT 14
ABP41194
ID ABP41194 standard; Protein; 169 AA.
XX
AC ABP41194;
XX
DT 23-AUG-2002 (first entry)
XX
DE Human ovarian antigen HTLHN94, SEQ ID NO:2326.
XX
KW Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
KW ovarian cancer; breast cancer; reproductive system disorder;
KW infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
KW PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection;
KW inflammatory condition; immune disorder; blood disorder;
KW cardiovascular disorder; respiratory disorder; neurological disorder;
KW gastrointestinal disorder; urinary system disorder; drug screening;
KW gene therapy; chromosome mapping; forensic analysis;
KW antibody preparation; cytostatic; immunomodulatory; neuroprotective;
KW antiinflammatory; gynaecological; reproductive.
XX
XX Homo sapiens.
OS
XX
PN WO200200677-A1.
XX
PD 03-JAN-2002.
XX
PF 07-JUN-2001; 2001WO-US18569.
XX
PR 07-JUN-2000; 2000US-209467P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Birse CE, Rosen CA;
XX
DR WPI; 2002-147878/19.
DR N-PSDB; ABO54271.
XX
PT Isolated nucleic acid molecules encoding novel ovarian polypeptides,
PT useful in the prevention, treatment and diagnosis of cancer (e.g.
PT ovarian cancer), immune disorders, cardiovascular disorders and
PT neurological diseases -
XX
PS Claim 11; SEQ ID NO 2326; 2922pp; English.
XX
CC The invention relates to 2175 novel human ovarian antigens (ABP41054-
CC ABP43228) and to cDNAs encoding them (ABO54131-ABO56305), and also
CC encompasses polypeptides 90% identical and polynucleotides 95% identical
CC to the sequences of the invention. The invention additionally relates to
CC recombinant vectors and host cells comprising human ovarian antigen
CC polynucleotides, antibodies against human ovarian antigens, and the use
CC of ovarian antigen polynucleotides and polypeptides in diagnosing,
CC treating, prognosing or preventing various ovary and/or breast-related
CC disorders. Such conditions include ovarian cancer and breast cancer, and
CC metastatic tumours of ovarian or breast origin, reproductive system
CC disorders (e.g., infertility, disorders of pregnancy, anovulation,
CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine
CC disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic
CC shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and
CC vaginitis), immune disorders (e.g., congenital and acquired
CC immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),

CC blood-related disorders (e.g., anaemia), cardiovascular disorders,
CC respiratory disorders, neurological disorders, gastrointestinal disorders
CC and urinary system disorders. Ovarian antigen polypeptides and
CC polynucleotides may also be used in screening for compounds which
CC modulate ovarian antigen expression or activity. The polynucleotides may
CC further be used for gene therapy, chromosome mapping, in the
CC identification of individuals and in forensic analysis, and the
CC polypeptides may be used as food additives or to prepare antibodies
CC useful in disease diagnosis, drug targeting and phenotyping. The present
CC sequence represents a human ovarian antigen of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 169 AA;
Query Match 25.0%; Score 239.5; DB 23; Length 169;
Best Local Similarity 37.3%; Pred. No. 5e-17;
Matches 47; Conservative 35; Mismatches 39; Indels 5; Gaps 2;
QY 64 LKANPEKRICRVFSTSPAKDSLSFEDFLDLVSFSDTATPDIKSHYAFRIFFDDGTI 123
Db 47 LQENPKERIVAAFS-EDGEGLTFNDFVDMFVLCESAPRELKANYAFKIYDFNDNF 105
QY 124 NREXLSRLVNCLTGEGEDTRLASASEMKQOLIDNILEESDIDRDGTINLSEFOHVISRSPD 183
Db 106 CKEDLELTARLT---KSELDDEEVVLVCDKVIIEADLDGDKLGAFDFEDMTAKAPDF 161
QY 184 ASSFKI 189
Db 162 LSTFHI 167
RESULT 15
AA11976
ID AA11976 standard; Protein; 120 AA.
XX
AC AA11976;
XX
DT 18-JUN-1999 (first entry)
XX
DE Human 5' EST secreted protein SEQ ID NO: 576.
XX
KW Human; secreted protein; EST; expressed sequence tag; diagnosis;
KW forensic; gene therapy; chromosome mapping; signal peptide; prostate;
KW upstream regulatory sequence; cytokine activity; cell proliferation;
KW differentiation; haematopoiesis regulation; tissue growth regulation;
KW reproductive hormone regulation; chemotactic; chemokinetic; haemostatic;
KW thrombolytic; anti-inflammatory; tumour inhibition.
XX
OS Homo sapiens.
XX
PN WO9906550-A2.
XX
PD 11-FEB-1999.
XX
PF 31-JUL-1998; 98WO-IB01232.
XX
PR 01-AUG-1997; 97US-0905144.
XX
PA (GEST) GENSET.
XX
PI Duclert A, Dumas Milne Edwards J, Lacroix B;
XX
DR WPI; 1999-153780/13.
DR N-PSDB; AAX40698.
XX
PT New isolated prostate-derived nucleic acids - used to develop
PT products which may have cytokine, immune regulatory, haematopoiesis
PT regulating, anti-inflammatory or tumour inhibition activity
XX
PS Claim 34; Page 664; 675pp; English.
XX

XX

Matches	43	Conservative	0	Mismatches	0	Indels	0	Gaps	0
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GenCore version 5.1.3
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Searched: 120991 seqs, 19878514 residues

Total number of hits satisfying chosen parameters: 120991

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	945	98.7	191	US-10-109-885-2	Sequence 2, Appl1
3	340	35.5	187	US-09-802-116-2	Sequence 2, Appl1
4	185.5	19.4	170	US-10-109-885-3	Sequence 3, Appl1
5	178.5	18.7	195	US-09-999-602-3	Sequence 3, Appl1
6	173.5	18.1	195	US-09-999-602-4	Sequence 4, Appl1
7	142	14.8	220	US-09-350-874-26	Sequence 26, Appl1
8	137	14.3	216	US-09-350-874-6	Sequence 6, Appl1
9	137	14.3	220	US-09-350-874-24	Sequence 24, Appl1
10	137	14.3	227	US-09-350-874-8	Sequence 8, Appl1
11	137	14.3	227	US-09-350-874-10	Sequence 10, Appl1
12	137	14.3	245	US-09-350-874-4	Sequence 4, Appl1
13	137	14.3	252	US-09-350-874-20	Sequence 20, Appl1
14	137	14.3	270	US-09-350-874-14	Sequence 14, Appl1
15	136	14.2	216	US-09-965-528-15	Sequence 15, Appl1
16	136	14.2	216	US-09-350-874-2	Sequence 2, Appl1
17	135.5	14.2	214	US-09-999-602-1	Sequence 1, Appl1
18	134	14.0	270	US-09-350-874-18	Sequence 18, Appl1
19	132	13.8	225	US-09-350-874-30	Sequence 30, Appl1

20	132	13.8	252	10	US-09-350-874-22	Sequence 22, Appl1
21	132	13.8	252	10	US-09-350-874-28	Sequence 28, Appl1
22	132	13.8	252	10	US-09-350-874-42	Sequence 42, Appl1
23	132	13.8	257	10	US-09-350-874-16	Sequence 16, Appl1
24	122	12.7	229	10	US-09-350-874-70	Sequence 70, Appl1
25	122	12.7	233	10	US-09-350-874-49	Sequence 49, Appl1
26	122	12.7	250	10	US-09-350-874-72	Sequence 72, Appl1
27	112.5	11.8	172	12	US-10-109-885-4	Sequence 4, Appl1
28	112.5	11.8	1210	9	US-10-025-380-692	Sequence 692, App
29	112.5	11.8	1210	10	US-09-922-217-692	Sequence 692, App
30	112.5	11.8	1210	10	US-09-833-263-692	Sequence 692, App
31	112.5	11.8	1548	9	US-10-025-380-1095	Sequence 1095, Ap
32	112.5	11.8	1548	10	US-09-922-217-1095	Sequence 1095, Ap
33	111	11.6	256	10	US-09-350-874-32	Sequence 32, Appl1
34	110.5	11.5	142	10	US-09-910-071-4	Sequence 4, Appl1
35	109	11.4	642	9	US-09-554-000-2	Sequence 2, Appl1
36	109	11.4	642	9	US-09-554-000-6	Sequence 6, Appl1
37	109	11.4	652	9	US-09-554-000-4	Sequence 4, Appl1
38	109	11.4	656	9	US-09-554-000-8	Sequence 8, Appl1
39	108	11.3	256	10	US-09-350-874-36	Sequence 36, Appl1
40	107.5	11.2	201	10	US-09-925-297-714	Sequence 714, App
41	106.5	11.1	159	10	US-09-910-071-5	Sequence 5, Appl1
42	103	10.8	203	10	US-09-350-874-12	Sequence 12, Appl1
43	101.5	10.6	139	10	US-09-864-761-34808	Sequence 34808, A
44	95.5	10.0	171	9	US-09-981-353-161	Sequence 161, App
45	94.5	9.9	90	10	US-09-826-589-3	Sequence 3, Appl1

ALIGNMENTS

RESULT 1:
US-09-878-454A-2
Sequence 2, Application US/09878454A
Patent No. US20020064828A1
GENERAL INFORMATION:
APPLICANT: Monteliro, et al.
TITLE OF INVENTION: Method of Controlling the Binding of Calmyrin to Presentl11r
FILE REFERENCE: 4115-161
CURRENT APPLICATION NUMBER: US/09/878,454A
PRIOR APPLICATION NUMBER: 2001-06-11
PRIOR FILING DATE: 2000-06-11
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 191
TYPE: PRT
ORGANISM: Homo sapiens
US-09-878-454A-2

Query Match	100.0%	Score 957;	DB 10;	Length 191;
Best Local Similarity	99.5%;	Pred. No. 3.4e-85;		
Matches 190;	Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MGGSGSRSLKELLAELYODLTFLTKQETLLAHRRCCELLPQEQRYESSLRAQVPFEQILS 60		
Db	1	MGGSGSRSLKELLAELYODLTFLTKQETLLAHRRCCELLPQEQRYESSLRAQVPFEQILS 60		
QY	61	LPFLKANPFRKICRVFSTSPAKDSLSFEFDLLSVFSDFATPDIKSHYAFRIFDDEDD 120		
Db	61	LPFLKANPFRKICRVFSTSPAKDSLSFEFDLLSVFSDFATPDIKSHYAFRIFDDEDD 120		
QY	121	GTLNREXLSRLVNCITGEGEDTRLSASEMKQILDNILESDIDRDGTINLSEFQHYISRS 180		
Db	121	GTLNREXLSRLVNCITGEGEDTRLSASEMKQILDNILESDIDRDGTINLSEFQHYISRS 180		
QY	181	PDFASSFKIVL 191		
Db	181	PDFASSFKIVL 191		

RESULT 2

US-10-109-885-2
; Sequence 2, Application US/10109885
; Patent No. US20020119129A1
; GENERAL INFORMATION:

; APPLICANT: REVEL, Michel
; APPLICANT: CHEBATH, Judith
; APPLICANT: ABRAMOVITCH, Carolina
; TITLE OF INVENTION: NOVEL IFN RECEPTOR I BINDING PROTEIN, DNA ENCODING THEM, AND METH
; TITLE OF INVENTION: MODULATING CELLULAR RESPONSE TO INTERFERON
; FILE REFERENCE: REVEL-14A
; CURRENT APPLICATION NUMBER: US/10/109,885
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: US/09/341,640
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: PCT/US98/00671
; PRIOR FILING DATE: 1998-01-15
; PRIOR APPLICATION NUMBER: US 60/035,636
; PRIOR FILING DATE: 1997-01-15
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 191
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-109-885-2

Query Match 98.7%; Score 945; DB 12; Length 191;
Best Local Similarity 98.4%; Pred. No. 4.9e-84;
Matches 188; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGGGSRSLSKELLAAYQDLTFLTKQELLAHRRFCELLPQEQRTVLESSLRAQVPFEQILS 60
Db 1 MGGGSRSLSKELLAAYQDLTFLTKQELLAHRRFCELLPQEQRSVLESSLRAQVPFEQILS 60
QY 61 LPELKANPFRICRVFSTSPAKDSLSFEDFLDLSVFSATPDIKSHYAFRIFDFFDD 120
Db 61 LPELKANPFRICRVFSTSPAKDSLSFEDFLDLSVFSATPDIKSHYAFRIFDFFDD 120
QY 121 GTLNREXLSRLVCLTGEGETRLSASEMKQLIDNILEESDIDRDGTINLSEFQHVISRS 180
Db 121 GTLNREXLSRLVCLTGEGETRLSASEMKQLIDYILEESDIDRDGTINLSEFQHVISRS 180
QY 181 PDFASSEFKIVL 191
Db 181 PDFASSEFKIVL 191

RESULT 3
US-09-802-116-2
; Sequence 2, Application US/09802116
; Patent No. US20020082406A1
; GENERAL INFORMATION:

; APPLICANT: Mathur, Brian
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. US20020082406A1 Human Kinase Interacting Protein and Polynu
; TITLE OF INVENTION: the Same
; FILE REFERENCE: LEX-0146-USA
; CURRENT APPLICATION NUMBER: US/09/802,116
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 60/187,719
; PRIOR FILING DATE: 2000-03-08
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 187
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-802-116-2

Query Match 35.5%; Score 340; DB 10; Length 187;
Best Local Similarity 39.9%; Pred. No. 9.7e-26;
Matches 77; Conservative 43; Mismatches 61; Indels 12; Gaps 5;

QY 1 MGGGSRSLSKELLAAYQDLTFLTKQELLAHRRFCELLPQ----EQRTVLESSLRAQVPFE 56
Db 1 MGNKQVTFTHEQLEAYQDCTFTTRKEINRLFYRYQDLAPQLVPLDYTTCPD---VKVPYE 57
QY 57 QILSLPELKANPFRICRVFSTSPAKDSLSFEDFLDLSVFSATPDIKSHYAFRIFD 116
Db 58 LIGSMPELKDNPFRQRIQAVFS-EDGDGHTLDNFDLDMFSVMSEMAPRDLKAYYAFKIYD 116
QY 117 FDDDGTLNREXLSRLVCLTGEGETRLSASEMKQLIDNILEESDIDRDGTINLSEFQHV 176
Db 117 FNNDDYICAWDLEQTVTKLT-RGE---LSAEVSLVCEKVLDEADGDHGRLSLEDFQNM 172
QY 177 ISRSPDFASSFKI 189
Db 173 ILRAPDFELSTFHI 185

RESULT 4
US-10-109-885-3
; Sequence 3, Application US/10109885
; Patent No. US20020119129A1
; GENERAL INFORMATION:
; APPLICANT: REVEL, Michel
; APPLICANT: CHEBATH, Judith
; APPLICANT: ABRAMOVITCH, Carolina
; TITLE OF INVENTION: NOVEL IFN RECEPTOR I BINDING PROTEIN, DNA ENCODING THEM, AND
; TITLE OF INVENTION: MODULATING CELLULAR RESPONSE TO INTERFERON
; FILE REFERENCE: REVEL-14A
; CURRENT APPLICATION NUMBER: US/10/109,885
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: US/09/341,640
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: PCT/US98/00671
; PRIOR FILING DATE: 1998-01-15
; PRIOR APPLICATION NUMBER: US 60/035,636
; PRIOR FILING DATE: 1997-01-15
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-10-109-885-3

Query Match 19.4%; Score 185.5; DB 12; Length 170;
Best Local Similarity 31.1%; Pred. No. 6.6e-11;
Matches 38; Conservative 32; Mismatches 47; Indels 5; Gaps 2;

QY 56 EQILSLPELKANPFRICRVFSTSPAKDSLSFEDFLDLSVFSATPDIKSHYAFRIF 115
Db 41 EEFMSLPQLQNPLVQRVIDIFDTD-GNGEVDFKEFIEGVQSQSVKGDKEQKLRFARIY 99
QY 116 DFDDGTLNREXLSRLVCLTGEGETRLSASEMKQLIDNILEESDIDRDGTINLSEFQHV 175
Db 100 DMDKDGYSINGELFQVLKMMVG---NNLKDQLQQLQIVDKTINADKDGGRISFEFCA 155
QY 176 VI 177
Db 156 VV 157

RESULT 5
US-09-999-602-3
; Sequence 3, Application US/099999602
; Patent No. US20020091084A1
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti G.
; APPLICANT: Corley, Neil C.
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: HUMAN CALCIUM BINDING PROTEIN
; FILE REFERENCE: PF-0468-2 CON

```

: CURRENT APPLICATION NUMBER: US/09/999,602
: CURRENT FILING DATE: 2001-10-25
: PRIOR APPLICATION NUMBER: 09/010,378
: PRIOR FILING DATE: 1998-01-21
: NUMBER OF SEQ ID NOS: 4
: SOFTWARE: PERL Program
: SEQ ID NO 3
: LENGTH: 195
: TYPE: PRT
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: OTHER INFORMATION: Incyte ID No. US20020091084A1
US-09-999-602-3

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Query Match      18.7%; Score 178.5; DB 10; Length 195;
Best Local Similarity 26.7%; Pred. No. 3.8e-10;
Matches 52; Conservative 36; Mismatches 78; Indels 29; Gaps 6;

QY      1 MGGSGSRLSK-ELLAEYQDITFLTKOEILLAHRRFCCELLPQQRTVSSSLRAQVPFEQIL 59
      11  | | : | | | : | : | : | | | | | |
Db      1 MGSRASTLLRDELEIEIKKETGFSSHQSITRLYSRFTSLDKGNGTLLSR-----EDFQ 52

QY      60 SLPELKANPFKERICRVFSTSPAKDSLSFEDFLDLVSF-----SDATPDP----- 105
      11  | | | | : | | | | : | : | | | : | : |
Db      53 RIPELAINPLGDIRINAF-FSEGEDQVNFRCGFMRITLAHRPIEDNEKSQDVNGPEPLNSR 111

QY      106 -IKSHYAFRIFFEDDDGTLNREXLSRLVNCLTGEGEDTRLSASEMKQILDNILEESDIDR 164
      11  | | : | | : | | | : | : | : | : | : | : | : |
Db      112 SNKLHFAFRFLYDLDDKDDKISRDELLQVLRMMVG-----VNISDEQLGIADRTIQEADQDG 167

QY      165 DGTINLSEFQHVISR 179
      11  | | : | | | : | : |
Db      168 DSAISFTTEFVAVLEK 182

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RESULT 6
US-09-999-602-4
; Sequence 4, Application US/09999602
; Patent No. US20020091084A1
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti G.
; APPLICANT: Corley, Neil C.
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: HUMAN CALCIUM BINDING PROTEIN
; FILE REFERENCE: PF-0468-2 CON
; CURRENT APPLICATION NUMBER: US/09/999,602
; CURRENT FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: 09/010,378
; PRIOR FILING DATE: 1998-01-21
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PERL Program
; SEQ ID NO 4
; LENGTH: 195
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20020091084A1 91706967
US-09-999-602-4

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Query Match          18.1%; Score 173.5; DB 10; Length 195;
Best Local Similarity 26.2%; Pred. No. 1.1e-09;
Matches 51; Conservative 36; Mismatches 79; Indels 29; Gaps 6;

QY      1 MGGSGSRLSK-ELLAEYODLTFLTKOEIILAHRRFCCLLPQEQRTVESSLRAQVPFEQIL 59
      11  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db      1 MGSRASTLLRDEELELEIKETGFSHSQITRLYSRFTSLDKGENTLSR-----EDFQ 52

QY      60 SLPELKANPEKERICRYVESTSPAKDSLSFEDFLDLLSVF-----SDTATPD----- 105
      :||| ||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db      53 RIPELAINPLGDRINAFPE-GEDQVNFRCGFMRITLAHFRPTEDNEKSKDVNGPEPLNSR 111

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QY 106 -IKSHYAFRIFEDDDGDTLNREXLSRLVNCLTGEGEDTRLASASEKOLIDNILEESDIDR 164
      | :|::||:| :|::||:| :|::||:| :|::||:| :|::||:| :|::||:| :|::||:|
Db 112 SNKLHEAFRLYPDLDKDEKISRDELLOVLRRMVG----VNISDEQLGSIADRTIQEADQDG 167
      | :|::||:| :|::||:| :|::||:| :|::||:| :|::||:| :|::||:| :|::||:|
QY 165 DGTINLSEFQHVISR 179
      | :|::||:| :|::||:| :|::||:| :|::||:| :|::||:| :|::||:| :|::||:|
Db 168 DSAISFTFEVKYLEK 182
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RESULT 7
US-09-350-874-26
; Sequence 26, Application US/09350874
; Patent No. US20020019020A1
; GENERAL INFORMATION:
; APPLICANT: Rhodes, Kenneth
; APPLICANT: An, Wenqian
; TITLE OF INVENTION: METHODS FOR TREATING CARDIOVASCULAR DISORDERS
; FILE REFERENCE: MNI-069
; CURRENT APPLICATION NUMBER: US/09/350,874
; EARLIER FILING DATE: 1999-07-09
; EARLIER APPLICATION NUMBER: USSN 60/110,277
; EARLIER FILING DATE: 1998-11-30
; EARLIER APPLICATION NUMBER: USSN 60/110,033
; EARLIER FILING DATE: 1998-11-25
; EARLIER APPLICATION NUMBER: USSN 60/109,333
; EARLIER FILING DATE: 1998-11-20
; EARLIER APPLICATION NUMBER: USSN 09/298,731
; EARLIER FILING DATE: 1999-04-23
; NUMBER OF SEQ. ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Simian sp.
US-09-350-874-26

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Query Match          14.8%; Score 142; DB 10; Length 220;
Best Local Similarity 23.4%; Pred. No. 1.5e-06;
Matches 43; Conservative 46; Mismatches 81; Indels 14; Gaps 5,
QY      11 ELLAEYQDITFLTKOEILLAHRRFCCELLPQEORTVESSLRAQVPEQILS--LPRLKAMP 68
        | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db       41 EGLEQLQEQTKFTRKELQVLRYGRFNKP-----SGIVNENEFQTYSQFFPGDSST 93
QY      69 EKERICRVESTSPAKDSLSEDFDLISVSFSDTATPDIKSHYAFRIFEDDDGTLNREXL 128
        : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db       94 YATFLFNADTN-HDGSVSFEDEFAGLSYL-RGTVDRLNWAFNLXDLNKDCITKEEM 151
QY     129 SRLVNC---LTGEGEDTRLASASEMKQILDNILLESDDIDRDGTINLSEFQHVISRSPDEAS 185
        :: : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db     152 LDIMKSIFYDMGKYTPALRREADPREHVENNFQKMDRNKDGVTYTEFTIESCQKDENIMR 211
QY     186 SFKI 189
        | : :
Db     212 SMOI 215

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RESULT 8
US-09-350-874-6
; Sequence 6, Application US/09350874
; Patent No. US20020019020A1
; GENERAL INFORMATION:
; APPLICANT: Rhodes, Kenneth
; APPLICANT: An, Wenqian
; TITLE OF INVENTION: METHODS FOR TREATING CARDIOVASCULAR DISORDERS
; FILE REFERENCE: MNI-069
; CURRENT APPLICATION NUMBER: US/09/350,874
; CURRENT FILING DATE: 1999-07-09
; EARLIER APPLICATION NUMBER: USSN 60/110,277
; EARLIER FILING DATE: 1998-11-30
; EARLIER APPLICATION NUMBER: USSN 60/110,033
; EARLIER FILING DATE: 1998-11-25
; EARLIER APPLICATION NUMBER: USSN 60/109,333

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Db      212 SMQL 215

RESULT 10
US-09-350-874-8
; Sequence 8, Application US/09350874
; Patent No. US20020019020A1
; GENERAL INFORMATION:
; APPLICANT: Rhodes, Kenneth
; APPLICANT: An, Wenqian
; TITLE OF INVENTION: METHODS FOR TREATING CARDIOVASCULAR DISORDERS
; FILE REFERENCE: MNI-069
; CURRENT APPLICATION NUMBER: US/09/350,874
; CURRENT FILING DATE: 1999-07-09
; EARLIER APPLICATION NUMBER: USSN 60/110,277
; EARLIER FILING DATE: 1998-11-30
; EARLIER APPLICATION NUMBER: USSN 60/110,033
; EARLIER FILING DATE: 1998-11-25
; EARLIER APPLICATION NUMBER: USSN 60/109,333
; EARLIER FILING DATE: 1998-11-20
; EARLIER APPLICATION NUMBER: USSN 09/298,731
; EARLIER FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Rattus sp.
US-09-350-874-8

Query Match      14.3%; Score 137; DB 10; Length 227;
Best Local Similarity 25.6%; Pred. No. 4.6e-06;
Matches 43; Conservative 35; Mismatches 76; Indels 14;

Qy      11 ELLAEYQDLTFLTKQEILLAHRRFCCELLPQEQTVESSLRAQVPFEQILS--LPELKA
      | | : : | | | | : : | | | | : : | | : : | | : : | | : : | | : : | |
Db      48 EGLEQLEAQTNFTKRELQVLYRGFKNECP-----SGVVNEETFKQIYAQFFPHGDA

Qy      69 FKERICRVFSTSPAKDSLSFEDFLDLLSVFSDTATPDIKSHYAFRIFDFDDGTLNRE
      : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | |
Db      101 YAHYLENAFDTTQT-GSVKPFEDFVTALSILL-RGTVHEKLRWTFNLYDINKDGYINKE

Qy      129 SRLVNC--LTGEGEDTRLASSEMQLIDNILEESDIDRDGTINLSEF 173
      : | : : | | : : | | : : | | : : | | : : | | : : | | : : | |
Db      159 MDIVKAIYDMGKYTPVLKEDTPRQHVDFVFQKMDKNKDGIVTLDEF 206

RESULT 11
US-09-350-874-10
; Sequence 10, Application US/09350874
; Patent No. US20020019020A1
; GENERAL INFORMATION:
; APPLICANT: Rhodes, Kenneth
; APPLICANT: An, Wenqian
; TITLE OF INVENTION: METHODS FOR TREATING CARDIOVASCULAR DISORDERS
; FILE REFERENCE: MNI-069
; CURRENT APPLICATION NUMBER: US/09/350,874
; CURRENT FILING DATE: 1999-07-09
; EARLIER APPLICATION NUMBER: USSN 60/110,277
; EARLIER FILING DATE: 1998-11-30
; EARLIER APPLICATION NUMBER: USSN 60/110,033
; EARLIER FILING DATE: 1998-11-25
; EARLIER APPLICATION NUMBER: USSN 60/109,333
; EARLIER FILING DATE: 1998-11-20
; EARLIER APPLICATION NUMBER: USSN 09/298,731
; EARLIER FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-350-874-10

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Db 144 YATFLNADTN-HDGSVSFEDEVAGLSVIL-RGTVDRLNWFNLYDLNKDGCITKEEM 201
QY 129 SRLVNC---LTGEGEDTRLASSEMKGQIDNILEESDIDRDGTINLSEFQHVISRSPDFAS 185
Db 202 LDIMKSIYDMGKYTPALREAPREHVESFFQKMDRKNKDGVTTEEFIESCQDENIMR 261
QY 186 SFKI 189
Db 262 SMOQL 265

RESULT 15
US-09-965-528-15
; Sequence 15, Application US/09965528
; Publication No. US20020187523A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: TANG, Y. Tom
; APPLICANT: YUE, Henry
; APPLICANT: LAL, Preeti
; APPLICANT: BURFORD, Neil
; APPLICANT: BANDMAN, Olga
; APPLICANT: BAUGHN, Maria R.
; APPLICANT: AZIMZAI, Yalda
; APPLICANT: LU, Dyung Aina M.
; APPLICANT: PATTERSON, Chandra
; TITLE OF INVENTION: EXTRACELLULAR SIGNALING MOLECULES
; FILE REFERENCE: PF-0701 USA
; CURRENT APPLICATION NUMBER: US/09/965,528
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/134,949
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 60/144,270
; PRIOR FILING DATE: 1999-07-15
; PRIOR APPLICATION NUMBER: 60/146,700
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: 60/157,508
; PRIOR FILING DATE: 1999-10-04
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PERL Program
; SEQ ID NO 15
; LENGTH: 216
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20020187523A1 3216587CD1
US-09-965-528-15

Query Match 14.2%; Score 136; DB 9; Length 216;
Best Local Similarity 25.6%; Pred. No. 5.4e-06;
Matches 43; Conservative 35; Mismatches 76; Indels 14; Gaps 5;

QY 11 ELLAEYQDLTFLTKQEILLAHRRFCELLPQEQRTVESSLRAQVPFEQILS--LPELKANP 68
Db 37 EGLEQLAQTNFTKRELQVLYRGFKNECP-----SGVVNEDTFKQIYAQFFPHGDAST 89
QY 69 FKERICRVFSTSPAKDSLSFEDFLDLSVFSDTATPDIKSHYAFRIFEDDDGDTLNREXL 128
Db 90 YAHYLENADFTTQT-GSVKFEDFVTALSILL-RGTVEKLRWTFNLYDINKDGYINKEEM 147
QY 129 SRLVNC---LTGEGEDTRLASSEMKGQIDNILEESDIDRDGTINLSEF 173
Db 148 MDIVKAIYDMGKYTPVLKEDTPRQHVDFVFFQKMDKKNKDGIVTLDEF 195

Search completed: January 17, 2003, 12:50:14
Job time : 12 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 17, 2003, 12:47:19 : Search time 17 Seconds
(without alignments)
1080.099 Million cell updates/sec

Title: MUT127
Perfect score: 957
Sequence: 1 MGGSGSRLSKELLAETQDLT.....EFQHVISRSPDPASSFKIVL 191

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	408	42.6	311	2	T21563 hypothetical prote
2	209.5	21.9	174	2	T41632 probable calcineur
3	203.5	21.3	175	2	JH0462 phosphoprotein pho
4	198.5	20.7	174	2	T47245 calcineurin regula
5	185.5	19.4	170	1	A33391 calcineurin regula
6	185.5	19.4	170	1	S34127 calcineurin regula
7	185.5	19.4	170	1	JC1220 calcineurin regula
8	185.5	19.4	216	1	S42716 calcineurin regula
9	182.5	19.1	369	2	T22708 hypothetical prote
10	177.5	18.5	170	2	JC5174 calcineurin regula
11	174.5	18.2	170	2	JC7242 calcineurin regula
12	173.5	18.1	170	2	A44307 calcineurin regula
13	171.5	17.9	179	2	JC1221 calcineurin regula
14	169.5	17.7	165	2	PS0261 calcineurin regula
15	169.5	17.7	176	2	JQ1232 calcineurin regula
16	169.5	17.7	195	2	T28047 hypothetical prote
17	169.5	17.3	213	2	T31775 hypothetical prote
18	165.5	17.3	190	2	T20725 calcineurin B-like
19	163.5	17.1	226	2	T51357 calcineurin B-like
20	155	16.2	190	2	T51686 frequenin - Africa
21	151.5	15.8	226	2	T08923 calcineurin B-like
22	150.5	15.7	213	2	T51356 calcineurin B-like
23	150	15.7	193	2	JH0816 gene Rem-1 protein
24	150	15.7	193	2	T05308 hypothetical prote
25	150	15.7	246	2	H85387 hypothetical prote
26	150	15.7	246	2	H85387 calcium-binding pr
27	149	15.6	193	2	T01375 calcium sensor hom
28	147	15.4	192	2	T01375 calcium sensor hom
29	144	15.0	190	2	A55666 neurocalcin - frui

30	141	14.7	191	2	JH0815	neural visinin-1lk
31	137.5	14.4	254	2	T29566	hypothetical prote
32	137	14.3	193	2	JC2186	hypocalcin - huma
33	137	14.3	270	2	JC7631	K+ channel-interac
34	136	14.2	224	2	F96668	protein FIN19.5 (1
35	134	14.0	193	2	JH0616	neurocalcin (clone
36	134	14.0	195	2	JC1347	hypocalcin - rat
37	133	13.9	190	2	S58303	related to neurona
38	133	13.8	191	2	JH0605	neural visinin-1lk
39	132	13.8	191	2	A48979	visinin-like prote
40	130.5	13.6	172	2	S38531	caltractin - mouse
41	129	13.5	791	2	A53691	diacylglycerol kin
42	128	13.4	190	2	S61168	hypothetical prote
43	127.5	13.3	172	2	I38424	centrin - human
44	126	13.2	214	2	T08922	hypothetical prote
45	125.5	13.1	202	2	S21155	recoverin - mouse

ALIGNMENTS

RESULT 1
T21563
hypothetical protein F30A10.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T21563
R:Barlow, K.
submitted to the EMBL Data Library, October 1996
A:Reference number: Z19442
A:Accession: T21563
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-311 <WILD>
A:Cross-references: EMBL:Z81072; PIDN:CAE03019.1; GSPDB:GN00019; CESP:F30A10.1
A:Experimental source: clone F30A10
C:Genetics:
A:Gene: CESP:F30A10.1
A:Map position: 1
A:Introns: 106/2; 139/3; 190/3; 240/1

Query Match
Best Local Similarity 42.6%; Score 408; DB 2; Length 311;
Matches 87; Conservative 42; Mismatches 52; Indels 26; Gaps 5;

QY 1 MGGSGSRLS-----KELLAETQDLTFLTKQELLAAHRRCELLPQEQRTVESS 48
DB 111 MGNMSSSLSELNLFSGKGVFTREQDLEQDCTFTFRKDIIRLYKRYALNPHK---VPTN 167
QY 49 LRAQVP-----FEQILSLPELKANPFRICRVFSTSPAKDSLFEDFLDLVSFSDTA 102
DB 168 MGNRPATITLTFEEVEKMPKLNPKRRICEVFS-EDGRGNLSEDFDLDFSVFSEMA 226
QY 103 TPDIKSHYAFRIFFDDDTLNREXLSRLVNCFTGEGEDTRLASSEMKOLIDNILESDI 162
DB 227 PLQLKLYAFRIYDYDGDDELGHDDLSKMRSLTRD---ELSDVEVEFTIERITEADL 282
QY 163 DRDGTINSEFQHVISRSPDFASSFKI 189
DB 283 DGDSSINFAEFHVSRSPDFIRTFHT 309

RESULT 2
T41632
probable calcineurin b subunit - fission yeast (Schizosaccharomyces pombe).
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 04-Feb-2000
C:Accession: T41632
R:McDougal, R.M.; Rajandream, M.A.; Barrell, B.G.; Ramsperger, U.; Pohl, T.
submitted to the EMBL Data Library, August 1999
A:Reference number: Z22005
A:Accession: T41632
A:Status: preliminary; translated from GB/EMBL/DBDJ

A;Experimental source: brain
C;Comment: With calcineurin catalytic chain plays an important role in neural and nonneu
C;Genetics:
A;Gene: PP2B-beta-1
C;Complex: heterodimer with calcineurin catalytic chain
C;Superfamily: calmodulin; calmodulin repeat homology
C;Keywords: blocked amino end; calcium binding; duplication; EF hand; heterodimer; lipop
F;2-170/Product: calcineurin regulatory chain #status predicted <MAT>
F;18-49/Domain: calmodulin repeat homology <EF1>
F;50-82/Domain: calmodulin repeat homology <EF2>
F;87-119/Domain: calmodulin repeat homology <EF3>
F;128-160/Domain: calmodulin repeat homology <EF4>
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted

Query Match 19.4%; Score 185.5; DB 1; Length 170;
Best Local Similarity 31.1%; Pred. No. 2.7e-07;
Matches 38; Conservative 32; Mismatches 47; Indels 5; Gaps 2;

QY 56 EQILSLPELKPANPKERICRVFSTSPAKDSLSFEFDLLSVFSDTATPDIKSHYAFRIF 115
Db 41 EEFMSLPQLQONPLVQRVIDIFDFTD-GNGEVDKFKEFIEGVQSQFSVKGDKQKLRFAFRIF 99

QY 116 DFDDGTLNREXLSRLVNCLTGEGEDTRLASSEMQLIDNILEESDIDRDGTINLSEFQH 175
Db 100 DMDKDGYSISNGELFQVLKMMVG-----NNLKDTQLQOIVDKTIINADKDGGRISFEFCA 155

QY 176 VI 177
Db 156 VV 157

RESULT 8
S42716
calcineurin regulatory chain, long splice form - rat
N;Alternate names: calcineurin beta subunit; calcineurin chain B; phosphoprotein phosph
N;Contains: calcineurin regulatory chain, short splice form
C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C;Accession: S42716; S42717
R;Chang, C.D.; Mukai, H.; Kuno, T.; Tanaka, C.
Biochim. Biophys. Acta 1217, 174-180, 1994
A;Title: cDNA cloning of an alternatively spliced isoform of the regulatory subunit of C
A;Reference number: S42716; MUID:94153993; PMID:8110831
A;Accession: S42716
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-216 <CHA1>
A;Cross-references: EMBL:D14425; NID:g286205; PIDN:BAA03318.1; PID:g286206
A;Accession: S42717
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 'M',48-216 <CHA2>
A;Cross-references: EMBL:D14568; NID:g286255; PIDN:BAA03422.1; PID:g286256
C;Complex: heterodimer with calcineurin catalytic chain
C;Superfamily: calmodulin; calmodulin repeat homology
C;Keywords: alternative splicing; blocked amino end; calcium binding; duplication; EF ha
F;2-216/Product: calcineurin regulatory chain, long splice form #status predicted <MATL>
F;48-216/Product: calcineurin regulatory chain, short splice form #status predicted <MAT
F;64-95/Domain: calmodulin repeat homology <EF1>
F;96-128/Domain: calmodulin repeat homology <EF2>
F;'M',48-216/Product: calcineurin regulatory chain, short splice form precursor #status
F;133-165/Domain: calmodulin repeat homology <EF3>
F;174-206/Domain: calmodulin repeat homology <EF4>
F;48/Modified site: myristylated amino end (Gly) (in mature form) #status experimental
F;49/Modified site: aspartic acid (Asn) #status predicted

Query Match 19.4%; Score 185.5; DB 1; Length 216;
Best Local Similarity 31.1%; Pred. No. 3.7e-07;
Matches 38; Conservative 32; Mismatches 47; Indels 5; Gaps 2;

QY 56 EQILSLPELKPANPKERICRVFSTSPAKDSLSFEFDLLSVFSDTATPDIKSHYAFRIF 115
Db 87 EEFMSLPQLQONPLVQRVIDIFDFTD-GNGEVDKFKEFIEGVQSQFSVKGDKQKLRFAFRIF 145

QY 116 DFDDGTLNREXLSRLVNCLTGEGEDTRLASSEMQLIDNILEESDIDRDGTINLSEFQH 175
Db 146 DMDKDGYSISNGELFQVLKMMVG-----NNLKDTQLQOIVDKTIINADKDGGRISFEFCA 201

QY 176 VI 177
Db 202 VV 203

RESULT 9
T22708
hypothetical protein F55C10.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T22708
R;Dobson, R.
submitted to the EMBL Data Library, June 1996
A;Reference number: Z19603
A;Accession: T22708
A;Status: preliminary; translated from GB/EMBL/DBBJ
A;Molecule type: DNA
A;Residues: 1-369 <WIL>
A;Cross-references: EMBL:Z74036; PIDN:CAA98489.1; GSPDB:GN00023; CESP:F55C10.1
A;Experimental source: clone F55C10
C;Genetics:
A;Gene: CESP:F55C10.1
A;Map position: 5
A;Introns: 159/2; 199/3; 213/1; 272/1; 312/3; 353/3

Query Match 19.1%; Score 182.5; DB 2; Length 369;
Best Local Similarity 27.8%; Pred. No. 1.2e-06;
Matches 50; Conservative 38; Mismatches 69; Indels 23; Gaps 6;

QY 3 GSGSRLSKELLAEQ--DLTFLTKQEILLAHRRCELLPQEQRTVSSSLRAQVFEQILS 60
Db 200 GADASLPMEMCSNFDAYELRLT-----RRFKKL-----DVDGS--GSLSVVEFMS 243

QY 61 LPELKPANPKERICRVFSTSPAKDSLSFEFDLLSVFSDTATPDIKSHYAFRIFDFFDD 120
Db 244 LPELQONPLVQRVIDIFD-EDNGEVDREFIQIGISQFSVKGDKNTKLKFAFRIFYDMDRD 302

QY 121 GTLNREXLSRLVNCLTGEGEDTRLASSEMQLIDNILEESDIDRDGTINLSEFQHVISRS 180
Db 303 GFISNGELFQVLKMMVG-----NNLKDSQLQOIVDKTILFHKDGDGKISQEFCDVVVEHT 358

RESULT 10
JC5174
calcineurin regulatory chain 2 - fruit fly (Drosophila melanogaster)
N;Alternate names: calcineurin beta subunit; calcineurin chain B-2; phosphoprotein 1
C;Species: Drosophila melanogaster
C;Date: 16-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 13-Aug-1999
C;Accession: JC5174
R;Warren, W.D.; Phillips, A.M.; Howells, A.J.
Gene 177, 149-153, 1996
A;Title: Drosophila melanogaster contains both X-linked and autosomal homologues of
A;Reference number: JC5174; MUID:97080515; PMID:8921860
A;Accession: JC5174
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-170 <WAR>
A;Cross-references: GB:U56245; NID:g1336009; PIDN:AAC47350.1; PID:g1336010
C;Comment: This protein is the calcium binding chain of calcineurin, involved in ca.
C;Genetics:
A;Gene: dCnB2
C;Complex: heterodimer with calcineurin catalytic chain
C;Superfamily: calmodulin; calmodulin repeat homology
C;Keywords: blocked amino end; calcium binding; duplication; EF hand; heterodimer;
F;2-170/Product: calcineurin regulatory chain #status predicted <MAT>
F;18-49/Domain: calmodulin repeat homology <EF1>
F;50-82/Domain: calmodulin repeat homology <EF2>
F;87-119/Domain: calmodulin repeat homology <EF3>

2,10-45/domain: calmodulin repeat homology <EF1>